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540 8 CCATGGTGGTGTCGATATCGGCAGTAGTCTTTGCCGAAACGTTGAGGGTTACAGTGATCTGCGTCGGACATACTTCGGGGAATCTACGGC GGAATATCAAAGTCTTCGGAATATCCATATTGGGAAAGGACAGAAGCTCCGGGGTAGTTTGATAGATGAGCTCCGGTGTATTAAATCGGG TGTTACATCTCTGGGCTACAGCTCGAGATGTGCCTGCCGAGTATACTTAGAAGCCATGCCAGCGTGTTGTTATACGACCAAAAGTCAGGG CATCCAACGGACTTCTCATACCACTCATTGACATATTTCAAACAGCTCCAGGCGCATTTAGTTCAACATGAAGCAATTCTCCGCCAAAC AGCTGACAGGAGTGAGCGTCATGTAGACCATCTAGTAATGTCAGTCGCGCGCAATTTCGCACATGAAACAAGTTGATTTCGGGACCCCAT ECHK! signal sequence Xmn I Sac 1 BssH II Bst1107 | Psp1406 I - oux EcoR V

F/G. 24

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F/G.\_3₿

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**F/G.**⊋८

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AGGGCGGACAGGGTGTGAATAATGCGCACACGACTTATTTTGGGATGACGAGCGGAGCCTGTACATGGTGATCAGTCATTTCAGCCTCCC	GGTGATCAGTCATTTCAGCCTCCC 1440	0
GAGTGTAC	BSPLU111	0
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EcoR V TGACAGATATCTCTAAACACCTTATCCGCTTAAACCCATCATAGATTGTGTCACGTGATAGACCCCTTGAATGATGAGAGCGAAATGTATCA	CTTGAATGATGAATGTATCA 1710	9
Sca I	Sca 1 Ppu10 1	0
GICCCGTITAAATCAAACCCTITCAGCCTAGCACAGICAGAATACACCCCAACCCCATTCTAAGGTAGTACTAAATATGAATACAGCCTAAA	GTACTAAATATGAATACAGCCTAAA 1800	00
Ear I Bgl II Sap I Nhe I	Nhe i Nco i Eco31 l	
TGCATCGCTATATGATCCCATAAAGAAGCAACAACCTTTCAGATCTCGTTTTGCGCTGCGAAGAGCTAGCT	CTAGCTCTACCATGGTCTCAATTAT 1890	90

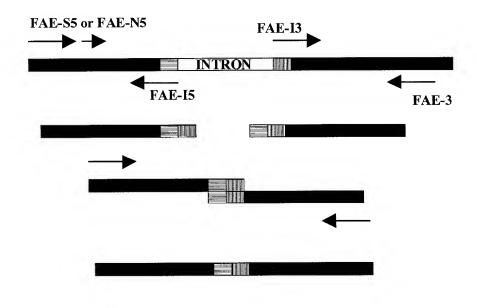
**FIG.**\_2 ₪

	BspLU111	BamH I Xma I Sma I	
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Xho I BseR I		_	
CTTCTTCACATCTCGAGGAGTTGTCTACACGTCGGGTCCATGTCATAAGCCGGTACTCGACGTTGTCGTGACCGTGACCCAGACCCCTGT	CATAAGCCGGTACTCGACGTTGTC	GTGACCGTGACCCAGACCCCTGT	2070
	Nco.	BsaB	_
TGATAGCGTTGAGAGGCCCTATATTTGAATTTCCAATCTCAG	CCAATCTCAGCTTTACGAAGATATGCCCATGGTGGAGGGTTAGTAAACCGATGATGA		2160
Eco311 Msc I	Bs	BspLU111	
; TCGTGTGCAGCATGAGATGAGACCGTGGCCAATCCTGTTCAAATGCCAAGACCCGCCTCCTACCACATGTAAGGCATCCGTCGGCCGCC	\TGCCAAGACCCGCCTCCTACCACA		2250
	Xcm I	Msc I BsrD I	_
GTTGAATTGTGCAAATGCCGAGATCATAAAAGCGGCCACACTTCCACGTCGGTACTGGATGGGTTGCGCGTGGCCATACTGTGTTTTCCA	TCCACGTCGGTACTGGATGGGTTGC		2340
Alwn I	Earl	Vsp.	
TTGCGTGGGTCGTTCGTGTTACTGCGACGCAGATTCTGTAGGCAAGGCGCAGGGCTCTTCTGAGGTAGAAAACACCCCATATTAATCT	CAAGGCGCAGGGCTCTCTTCTGAG		2430
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GAATTC 2436	יי <b>לו</b>		

**7/G.** ⊇ ⊏

CATGGTCTCAATTATGAGTGGAGCGTTTAGTCTCGTTTAAGCCTAGCTATCTTATAAGGACAACACATGTACATG **GGCTTACTTGTAGAGAGGTAGGATCCCGGGCTTCTTCACATCTCGAGGAGTTGTCTACACGTCGCGTCCATGTCA** CCGAAGACCTCTACAGCCGTTTAGTCGAAATGGCCACTATCTCCCAAGGTGCCTACGCCGACCTGTGCAACATTC TCACGCCTTTCGACACCCTACCACAATGCAACGGTTGTGAAGTACACGGTGGATATTATATTTGGATGGGTCTCCG **TCCAGGACCAAGTCGAGTCGCTTGTCAAACAGGTTAGCCAGTATCCGGACTATGCGCTGACTGTGACGGGCC ACAGGTATGCCCTCGTGATTTCTTTTAAGTGTGTATAATACTCACTAACTCTACGATAGTCTCGGAGCGTCCC** TGGCAGCACTCACTGCCGCCCAGCTGTCTGCGACATACGACAACATCCGCCTGTACACCTTCGGCGAACCGCGA GCGGCAATCAGGCCTTCGCGTCGTACATGAACGATGCCTTCCAAGCCTCGAGCCCAGATACGACGCAGTATTCC **GGGTCACTCATGCCAACGACGGCATCCCAAACCTGCCCCCGGTGGAGCAGGGGTACGCCCATGGCGGTGTAGAGT ACTGGAGCGTTGATCCTTACAGCGCCCAGAACACATTTGTCTGCACTGGGGATGAAGTGCAGTGCTGTGAGGCCC AGGGCGGACAGGGTGTGAATAATGCGCACACGACTTATTTGGGATGACGAGCGGAGCCTGTACATGGTGATCAG** GAGGTTGCCTTTCTCTTTTGATTGTGAATATATATTTAAGTAGATGACAGATATCTCTAAACACCTTATCCGCT **TAAACCCATCATAGATTGTGTCACGTGATAGACCCCCTTGAATGAGGCGAAATGTATCAGTCCCGTTTAAATCA AACCCTTTCAGCCTAGCACAGTCAGAATACACCCCCATTCTAAGGTAGTACTAAATATGAATACAGCCTAAA** TAAGCCGGTACTCGACGTTGTCGTGACCGTGACCCAGACCCCTGTTGATAGCGTTGAGAAGGCCCTATATTTGAA **TITCCAATCTCAGCTTTACGAAGATATGCCCCATGGTGGAGGGTTAGTAAACCGATGATGATCGTGTGCAGCATGA** GATGAGACCGTGGCCAATCCTGTTCAAATGCCAAGACCCGCCTCCTACCACATGTAAGGCATCCGTCGGCCGCAC GITGAATTGTGCAAATGCCGAGATCATAAAAGCGGCCACACTTCCACGTCGGTACTGGATGGGTTGCGCTGGCC ATACTGTGTTTTCCATTGCGTGGGTCGTTTCGTGTTACTGCGACGCAGATTCTGTAGGCAAGGCGCAGGGCTCTCT CGCGCGCAATTTCGCACATGAAACAAGTTGATTTCGGGACCCCATTGTTACATCTCGGCTACAGCTCGAATG TGCCTGCCGAGTATACTTAGAAGCCATGCCAGCGTGTTGTTATACGACCAAAAGTCAGGGAATATGAAACGATCG CATCCAACGGACTTCTCATACCACTCATTGACATATTTCAAACAGCTCCAGGCGCATTTAGTTCAACATGAAGC **AATTCTCCGCCAAACACGTCCTCGCAGTTGTGGTGACTGCAGGGCACGCCTTAGCAGCCTCTACGCAAGGCATCT CCATGGTGGTGTGTCGATATCGGCAGTAGTCTTTGCCGAAACGTTGAGGGTTACAGTGATCTGCGTCGGACATACTT** CGGGGGAATCTACGGCGGAATATCAAAGTCTTCGGAATATCCATATTGGGAAAGGACAGAAGCTCCGGGGTAGTTT GATAGATGAGCTCCGGTGTATTAAATCGGGAGCTGACAGGAGTGAGGCGTCATGTAGACCATCTAGTAATGTCAGT CTGAGGTAGAAAACACCCCATATTAATCTGAATTC

Figure <u></u>

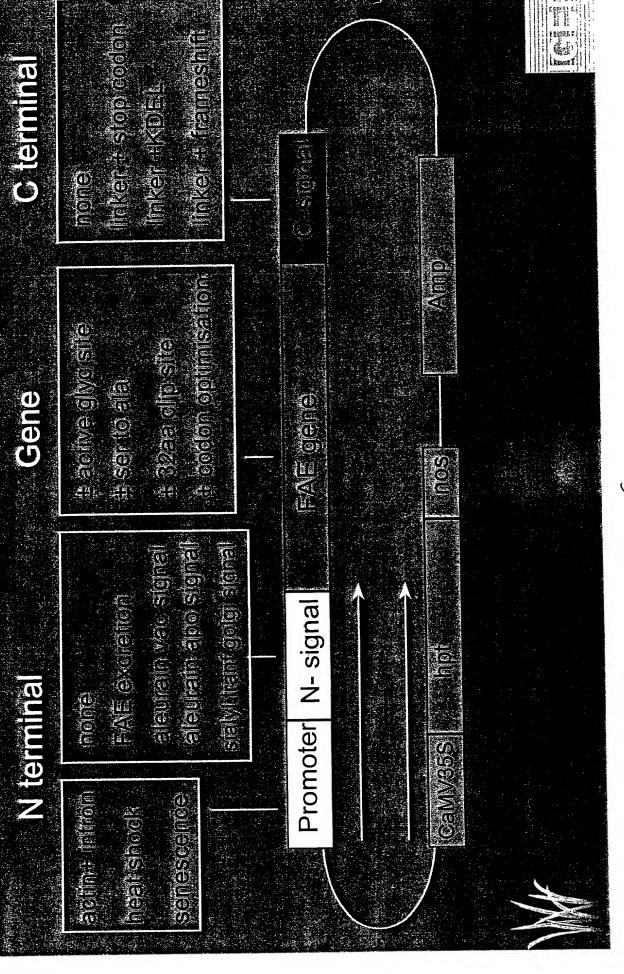


	40-mer
35-mer	
CCGGCCACGCCTCGGCCTCCCTGGCGGCACTC	GGCGCCGAGGGGGGCCGGTCACGGTCAGCGCGTAGTCC
FAE-I3	FAE-I5

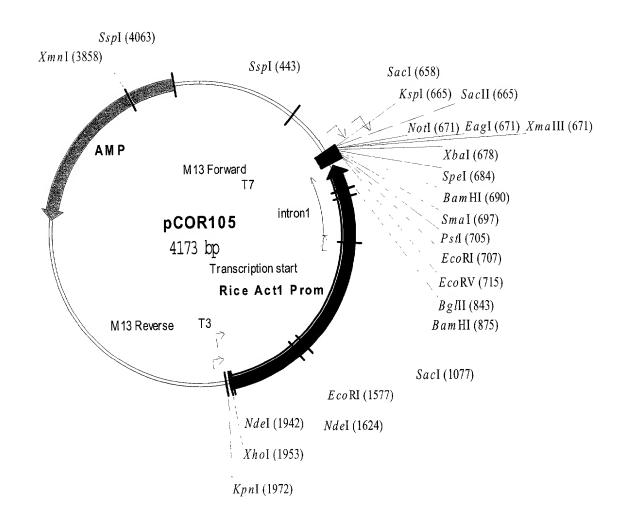
complement, FAE-I5 FAE-I3

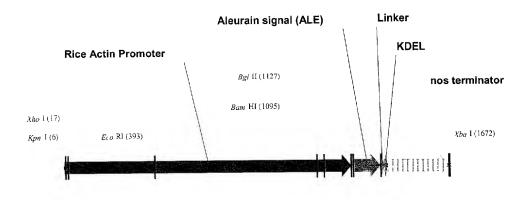
intron position in original

## Vector construction



### Figure \_\_\_\_\_





Hin dIII (1245) Hin dIII (1667)

Generic ALE-TER vector

1676 bp

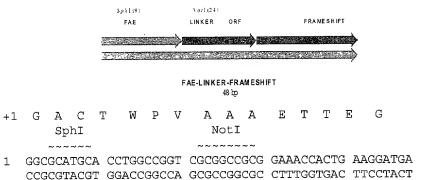
Neo I (1252) Not I (1372)

KDEL-COOH ER retention sequence

NotI

A A A K P L K D E L  $\star$  1 GCGGCCGCGA AACCACTGAA GGATGAGCTG TAA

### FAE-LINKER-FRAMESHIFT structure and sequence



## Plant transformation cassettes

* - Modified actin promoter (Kpn1-EcoR1 deletion and restored NCO site)	See1  B 8.1	3	hyg hyg 44 46 H6 45 X3 X3 X3 X3 C4.9 * C4.9 *	Target  VAC  APO  VAC  VAC  VAC  E.R.  E.R.  E.R.  APO  GOLGI  APO  VAC	ginal Actin + hyg	orig TR 9 TR6 TR6. *	HS HS
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			2002 2003 2003	And an analysis of the position of			
		ı	pJ06.3 *	VAC			
- * 8:90	7.55.57 4.53.04	ı	parco.4	A D			
Q3.2 * - 06.3 * -			÷	!			
Q3.2 * - 06.3 * -	ı	1	pJQ4.9 *	GOLGI			
Q4.9 * - Q3.2 * -	i	í	ı	APO		TR2	
TR2 - APO	ı	UK1	UF1	Щ Қ.		TR6.	TT2
TR6.1 — E.R. UF1 UK1  TR2 — MPO	1	UH11	0H9	ті Ж.	The special state is a complement of produce and special absences. The special	ı	ı
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TR6.1	ı		_			1	1
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TR6.1 — — — — — — — — — — — — — — — — — — —		c. c.	HOX3	VAC	And inches the second of the s	TR8 (	ı
TR8 (-glycos)  -	ı	10.7	0 > 0	(4)	Management of the control of the con	1	ı
TR8 (-glycos)	1	UK 6	UH5	VAC		•	ı
TR8 (-glycos)	1	UH13	0H7	APO		) ; )	
TR8 (-glycos)  TR6 (-glycos)  TR6.1  TR6.1  TR7  TR7  TR7  TR7  TR7  TR7  TR7  TR	ı	UH12	0He	APO		TT5.5	
TT5.5  TT8.6 (-glycos)  TR8 (-glycos)  TR6.1  TR6.1  TR7.  T	В 8.1		UH4	VAC	. 4	TR 9	TT3
TR 9.4 ———————————————————————————————————							N I
TR8 (-glycos)  TR6.1  TR6.1  TR7.2  TR6.1  TR7.2  TR7.2  TR7.3  T	1	1	μ/η + <i>/</i>		ainal Actin + hva	oric	
TT5.5  TT6.4  TT7.5  T	See1			•			ectors
Actin       H.S. in the hyginal Actin + hygin       Target       (+ hyginal Actin + hyginal +							

VAC

(ii)

### Vectors

### Original Actin promoter in pCOR105

J	Target	Signal sequences	Vectors
(i)	APO	- aleurain-NPGR-FAE	pUH6, pTT5, TT5.5, pTT5.1
(ii)	ER	<ul> <li>- aleurain-delNPIR -FAE</li> <li>- aleurain-NPGR-FAE-linker-KDEL</li> <li>- aleurain-delNPIR-FAE-linker-KDEL</li> </ul>	pUH7, pUA4.4, pTU5, pUH8, pUG4, pUH9,
(iii)	VAC	- aleurain-NPIR-FAE	pTP11.1, pTR9.4, pUH4, pUK3,
(iv)	ER/VAC	- aleurain-NPIR-FAE-linker-KDEL	pTU4, pUH3,
(v)	VAC	- aleurain-NPIR-FAE-linker-frameshift	pUA1K3, pTP3.1, pUC5.11
(vi)	VAC	- aleurain-NPIR-FAE-linker-stop	pTP8.5, pUH5
(vii)	ER	- Aspergillus signal -FAE-KDEL	pTP5.1, pTP6.1, pUF1,
Modif	ied actin pron	noter (Kpn1-EcoR1 deletion and restored	NCO site)
(i)	VAC	- aleurain-NPIR-FAE-linker-frameshift	рЈ06.3
(i) (ii)	GOLGI	- RST-FAE-linker-frameshift	pJQ3.2
(iii)	APO	- PPI-FAE-linker-frameshift	pJQ4.9
Heat-	shock promo	oter	
(i)	APO	- aleurain-NPGR-FAE - aleurain-delNPIR-FAE	pUH12 pUH13
		- Aspergillus signal-FAE	pTP4a2, pTR2.22,
(ii)	ER	<ul><li>- aleurain-NPGR-FAE-linker-KDEL</li><li>- aleurain-delNPIR-FAE-linker-KDEL</li></ul>	pUH10 pUH11
(:::)	MAC	- aleurain-NPIR-FAE-IIIREI-ADEL	pUK3,pTT3
(iii)	VAC ER/VAC	- aleurain-NYIR-FAE - aleurain-NPIR-FAE-linker-KDEL	pUK2
(iv) (v)	VAC	- aleurain-NPIR-FAE-linker-frameshift	pUC5.11, pHOX3
(v) (vi)	VAC	- aleurain-NPIR-FAE-linker-stop	pUK6
(vii)	ER	- Aspergillus signal -FAE-KDEL	pUK1, pTT2
Sene	escence prom	oter	
(i)	APO	- See1-PPI-FAE-linker-frameshift	pJQ5.2
(11)	VAC	Cool alouroin deleted NPIR-FAF	nIJR8 1

Figure 12

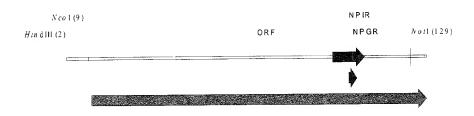
- See1-aleurain-deleted NPIR-FAE

pUB8.1



### ALEURAIN -NPIR (Vacuolar) and NPGR (Apoplast) structure and sequence

NPIR UNDERLINE
NPGR BOLD



### ALEURAIN-NPIR 134 bp

+1 MAHARVLLLALAVLATAAVA HindIII NcoI

AAGCTTACCA TGGCCCACGC CCGCGTCCTC CTCCTGGCGC TCGCCGTGCT GGCCACGGCC GCCGTCGCCG
TTCGAATGGT ACCGGGTGCG GGCGCAGGAG GAGGACCGCG AGCGGCACGA CCGGTGCCGG CGGCAGCGGC

+1 V A S S S S F A D S N P I R P V T D R A A NotI

71 TCGCCTCCTC CTCCTCCTTC GCCGACTCCA ACCCGATCCG GCCCGTCACC GACCGCGGG CCGC AGCGGAGGAG GAGGAAGG CGGCTGAGGT TGGGCTAGGC CGGCGAGTGG CTGGCGCGCC GGCG

### RAT SIALYL TRANSFERASE Golgi signal sequence

HindIII

- . V I C V W K K G S D Y E A L T L Q A K E F Q M . 71 CCGTGATCTG CGTGTGGAAG AAGGGCTCCG ACTACGAGGC CCTCACCCTC CAAGCCAAGG AGTTCCAAAT

NotI

· A A

141 GGCGGCCGC

### **Figure** <u>15</u>

### POTATO PROTEASE INHIBITOR II Apoplast signal sequence

HindIII

NcoI

· L V S A M E H V D A K A C T X E C G N L G F G ·

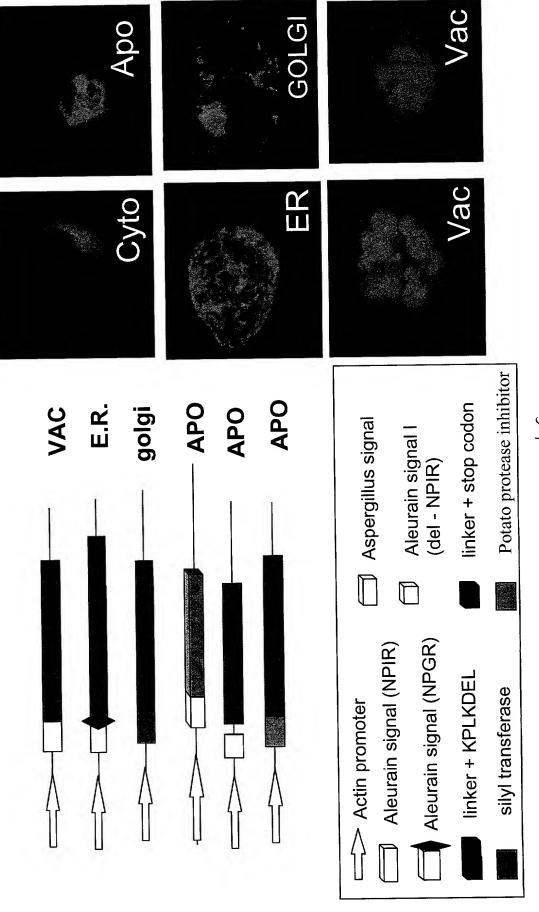
71 TGCTCGTSTC CGCCATGGAG CACGTGGACG CCAAGGCCTG CACCCKCGAG TGCGGCAACC TCGGCTTCGG

NotI

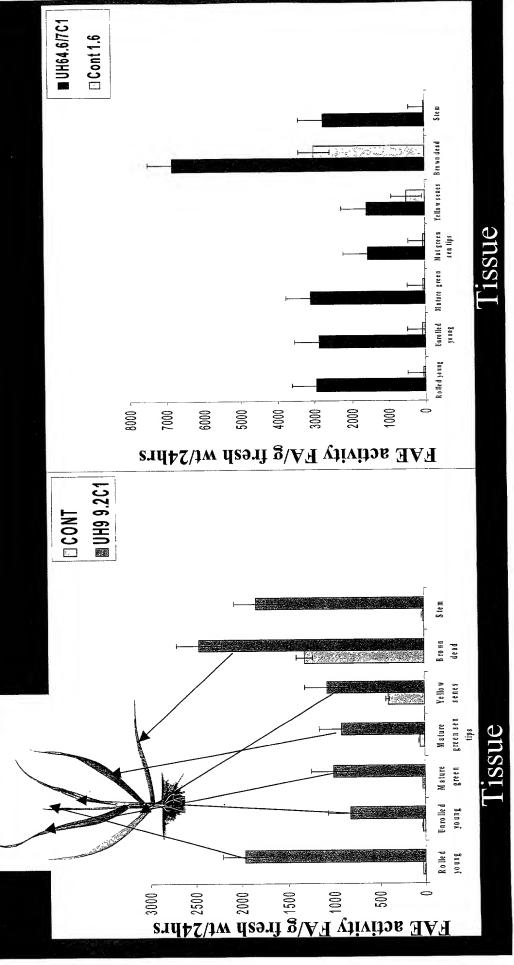
· I C P A A A
141 CATCTGCCCG GCGGCCGCC

### Targeting expression of grp to different cell compartments

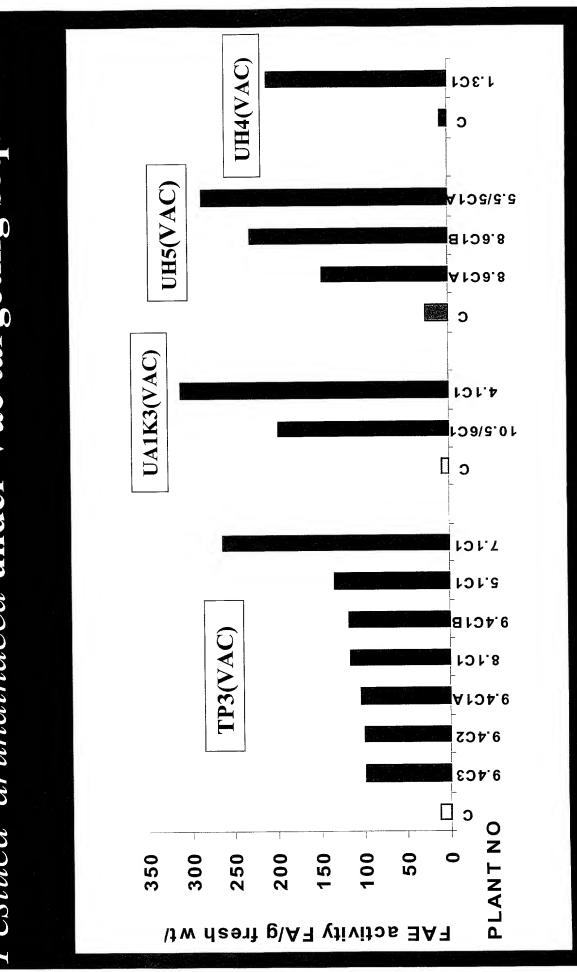
# Actin promoter targeting vectors



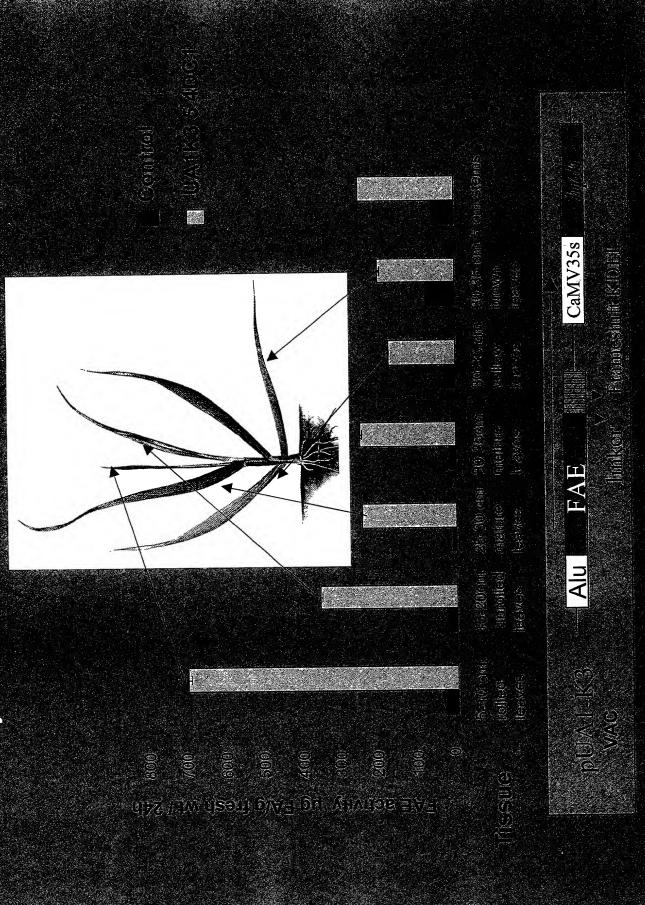
FAE activity in transgenic Festuca arundinacea leaves of different ages under ER and APO targeting sequence.



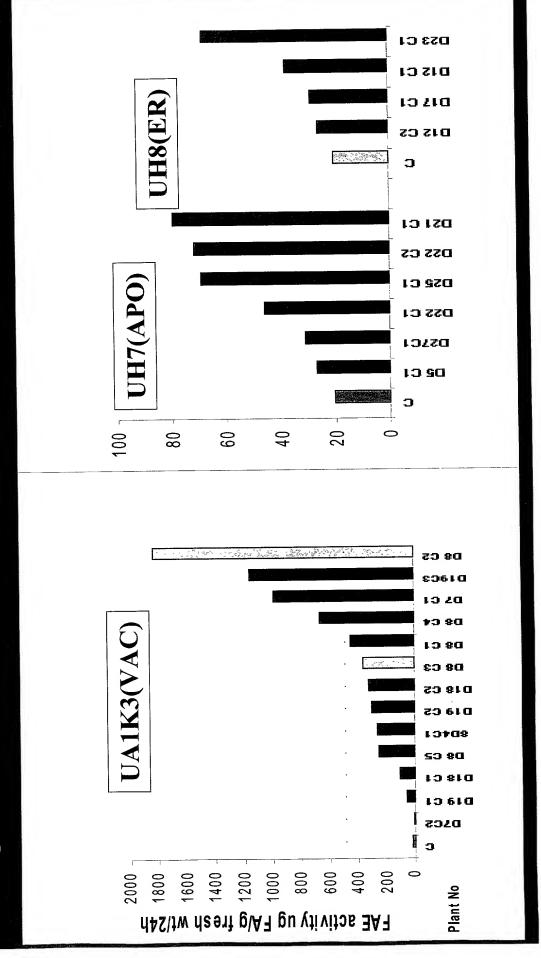
Fi our 6 17



FAE activity in Lollum mutiflorum leaves of different ages



FAE activity in leaves of primary transforman *lorum* under V targeting sequence. of Lolium multif



hydroxycinnamicacids in Festuca arundinacea plants expressing FAE under VAC targeting sequence. Levels of esterified monomeric and dimeric

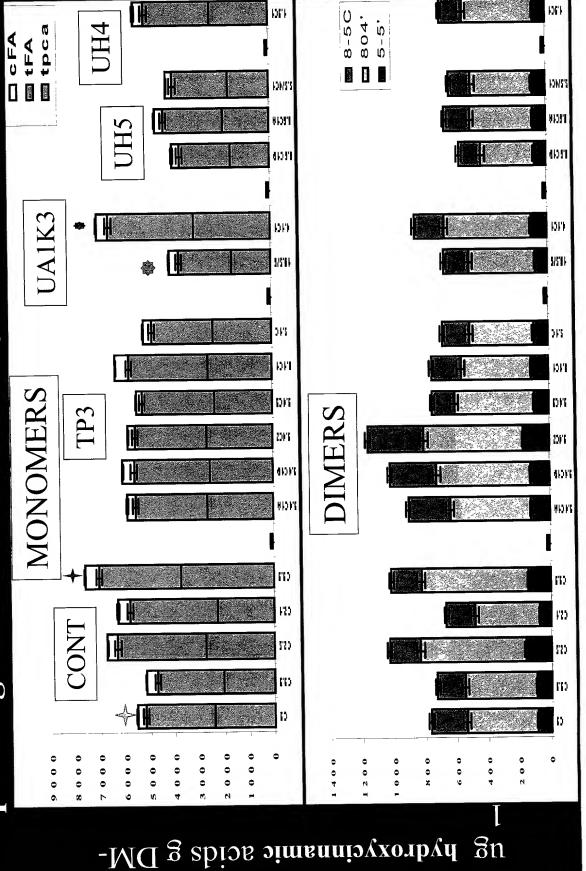
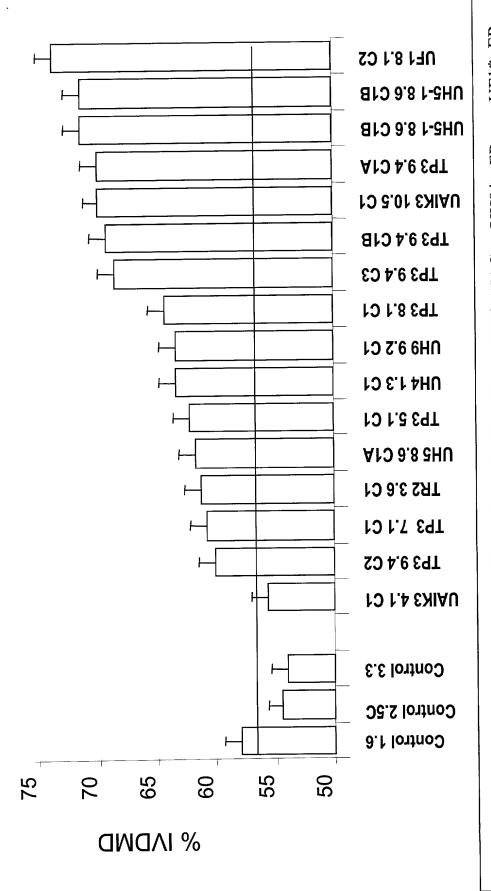


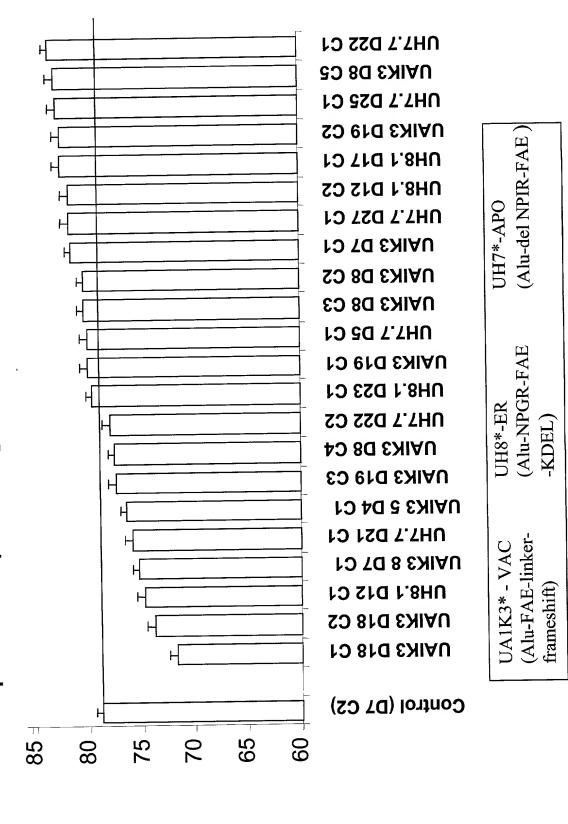
Figure 27

In vitro dry mater digestibility of leaf tissue of mature Festuca arundinacea plants expressing FAE under an actin promoter



(Asp-FAE-linker UF1\* -ER -KDEL) (Alu-delNPIRlinker-KDEL UH9\* - ER UH4\* -VAC CaMV-Hyg) (Alu-FAE+ UH5\* -VAC (Alu-FAElinker-stop \* co-integration vector 下、のなっと (Asp-FAE) TR2-APO (Alu-FAE-linker frameshift) TP3-VAC (Alu-FAE-linker-**UA1K3\* - VAC** frameshift)

In vitro dry mater digestibility of leaf tissue of mature Lolium multiflorum plants expressing FAE under an actin promoter



% INDWD

\* co-integration vector ド: タル・ヘスリ いっぱののので

Chimilding Car Production

50

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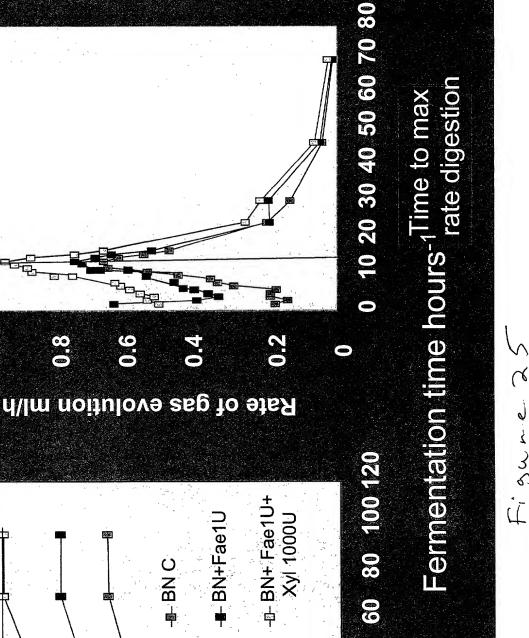
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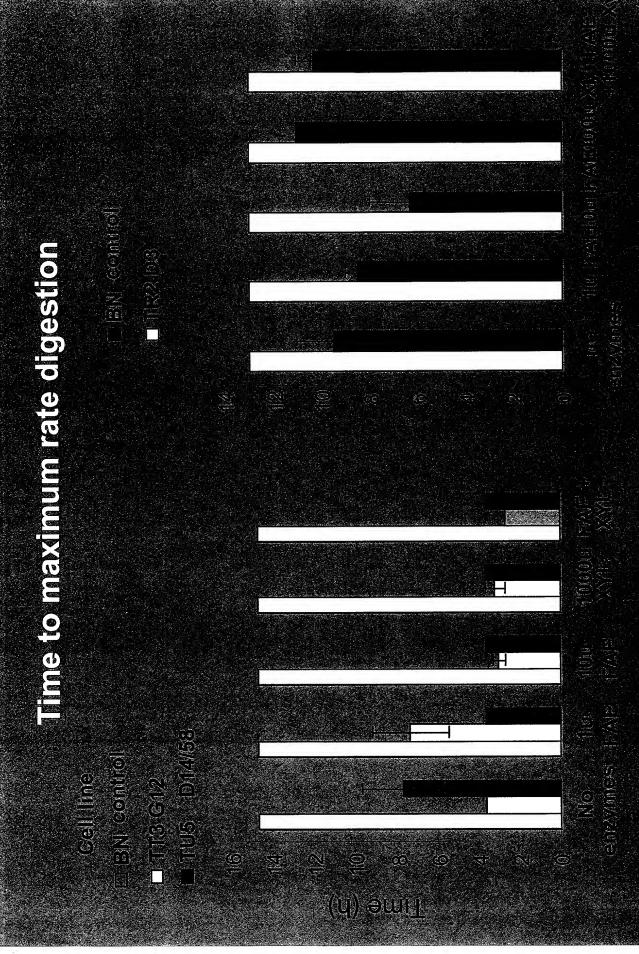
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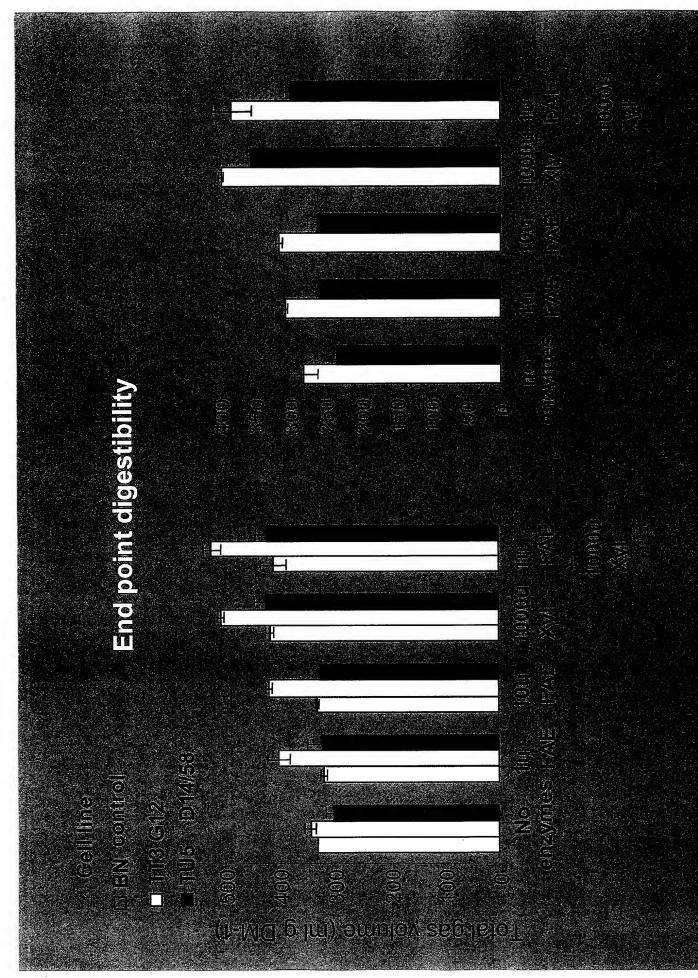
Fermentation time hours-<sub>1</sub>Time to max rate digestion

## In-vitro fermentation of Festuca arundinacea cell walls from eall cultures expressing recombinant FAE1









### Kinetics of FAE activity by ferulic acid release from cell wall under self digestion in Festuca arundinacea and stimulation by Xylanase.

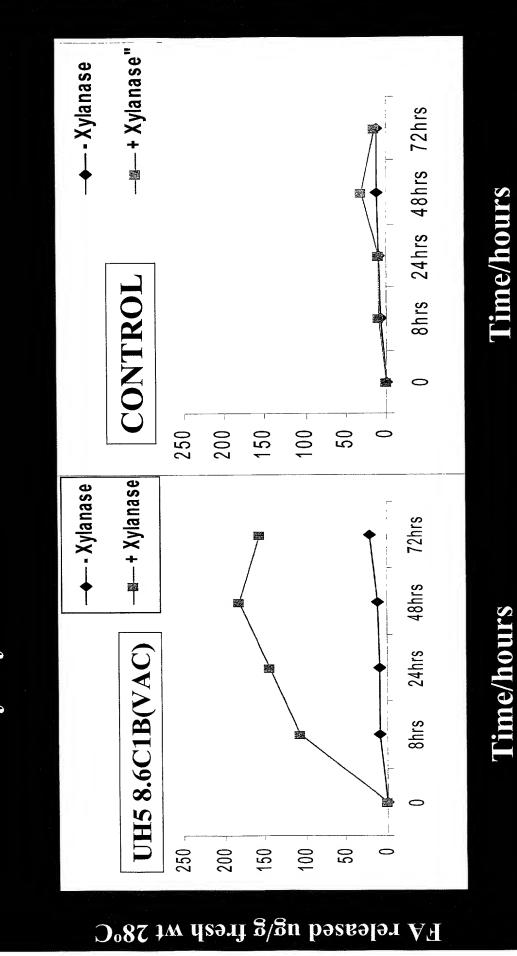
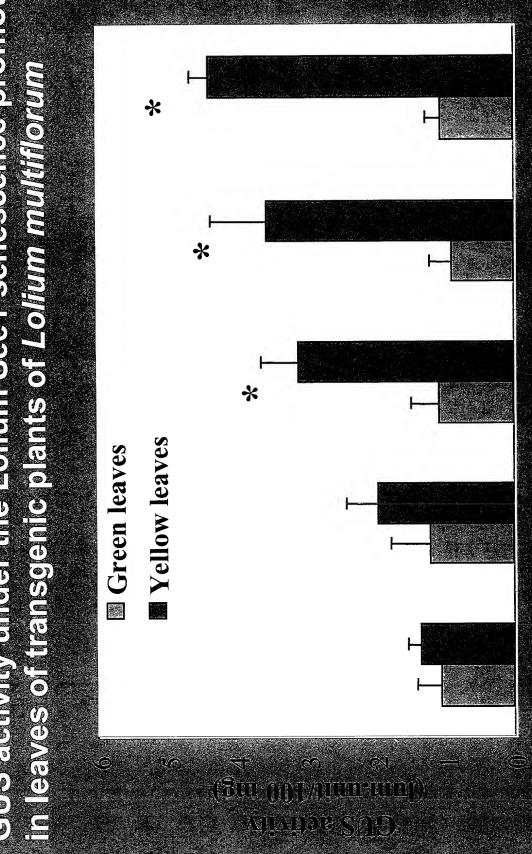
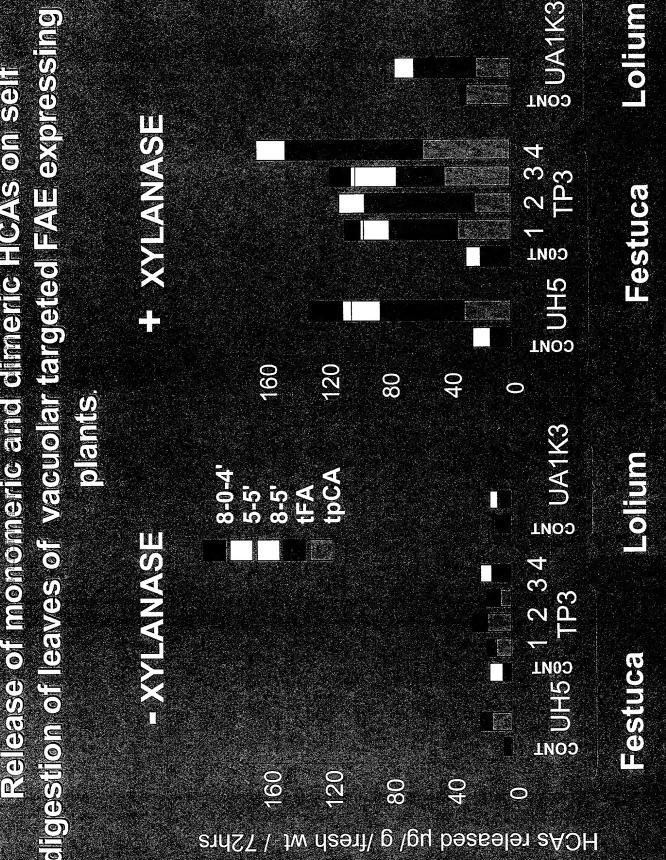


Figure 29



Figur &



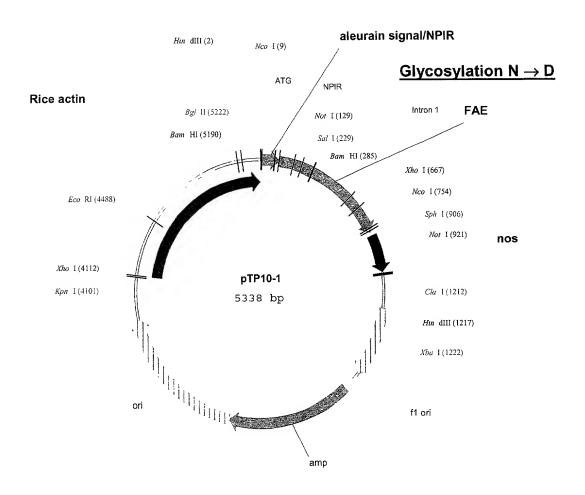


Figure 32A

### Figure 32 B

	Ncol
	HindIII
1	M A H A R V L L L A L A V L A T A A V A V A A A A A A A A A A A A A
	NPIR NotI
71	· A S S S S F A D S N P I R P V T D R A A A S T TCGCCTCCTC CTCCTCC GCCGACTCCA ACCCGATCCG GCCCGTCACC GACCGCGCGG CCGCCTCCAC · Q G I S E D L Y S R L V E M A T I S Q A A Y A GCAGGGCATC TCCGAAGACC TCTACAGCCG TTTAGTCGAA ATGGCCACTA TCTCCCAAGC TGCCTACGCC
	SalI
211	D L C N I P S T I I K G E K I Y N S Q T D I N G GACCTGTGCA ACATTCCGTC GACTATTATC AAGGGAGAGA AAATTTACAA TTCTCAAACT GACATTAACG
	BamHI
281	· W I L R D D S S K E I I T V F R G T G S D T N GATGGATCCT CCGCGACGAC AGCAGCAAAG AAATAATCAC CGTCTTCCGT GGCACTGGTA GTGATACGAA
	Glycosylation
351 421	· L Q L D T D Y T L T P F D T L P Q C N G C E V  TCTACAACTC GATACTGACT ACACCCTCAC GCCTTTCGAC ACCCTACCAC AATGCAACGG TTGTGAAGTA  H G G Y Y I G W V S V Q D Q V E S L V K Q Q V S  CACGGTGGAT ATTATATTGG ATGGGTCTCC GTCCAGGACC AAGTCGAGTC GCTTGTCAAA CAGCAGGTTA  · Q Y P D Y A L T V T G H X L G A S L A A L T A
491	GCCAGTATCC GGACTACGCG CTGACCGTGA CCGGCCACKC CCTCGGCGCC TCCCTGGCGG CACTCACTGC  · A O L S A T Y D N I R L Y T F G E P R S G N Q
561	CGCCCAGCTG TCTGCGACAT ACGACAACAT CCGCCTGTAC ACCTTCGGCG AACCGCGCAG CGGCAATCAG
	XhoI
631	A F A S Y M N D A F Q A S S P D T T Q Y F R V S GCCTTCGCGT CGTACATGAA CGATGCCTTC CAAGCCTCGA GCCCAGATAC GACGCAGTAT TTCCGGGTCA
	NcoI ~~~~~~
701	· H A N D G I P N L P P V E Q G Y A H G G V E Y CTCATGCCAA CGACGGCATC CCAAACCTGC CCCCGGTGGA GCAGGGGTAC GCCCATGGCG GTGTAGAGTA

A Q G G Q G V N N A H T T Y F G M T S G A C T V 841 GCCCAGGGCG GACAGGGTGT GAATAATGCG CACACGACTT ATTTTGGGAT GACGAGCGGC GCATGCACCT

. W S V D P Y S A Q N T F V C T G D E V Q C C E CTGGAGCGTT GATCCTTACA GCGCCCAGAA CACATTTGTC TGCACTGGGG ATGAAGTGCA GTGCTGTGAG

SphI

### Figure 32 C

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	· P V A				×		
911		GGCCGCGGAA					
981		TAAGATTGAA					
1051		AATAATTAAC					
1121	GCAATTATAC	ATTTAATACG	CGATAGAAAA	CAAAATATAG	CGCGCAAACT	AGGATAAATT	ATCGCGCGCG
			HindII				
			claI	.~ XbaI			
			~~~~	ADA1			
1191	GTGTCATCTA	TGTTACTAGA	TCGATAAGCT	TCTAGAGCGG	CCGGTGGAGC	TCCAATTCGC	CCTATAGTGA
1261		GCGCGCTCAC					
1331		TTGCAGCACA					
1401		GTTGCGCAGC					
1471		ACGCGCAGCG					
1541		TCGCCACGTT					
1611		TTTACGGCAC					
1681		ACGGTTTTTC					
1751		CACTCAACCC					
1821		AAATGAGCTG					
1891		CTTTTCGGGG					
1961		CATGAGACAA					
2031		CGTGTCGCCC					
2101		AAGTAAAAGA					
2171		GATCCTTGAG					
2241		GCGGTATTAT					
2311		TGGTTGAGTA					
2381		TGCCATAACC					
2451		ACCGCTTTTT					
2521		CCATACCAAA					
2591		TGGCGAACTA					
2661		CCACTTCTGC					
2731		CTCGCGGTAT					
2801		GAGTCAGGCA					
2871		TAACTGTCAG					
2941		TCTAGGTGAA					
3011		GTCAGACCCC					
3081		CAAACAAAAA					
3151		AGGTAACTGG					
3221		CTTCAAGAAC					
3291		GGCGATAAGT					
3361		GAACGGGGGG					
3431		TGAGCTATGA					
3501		GGAACAGGAG					
3571		GCCACCTCTG					
3641		CAACGCGGCC					
3711		CCTGATTCTG					
3711		AGCGCAGCGA					
3851		GCCGATTCAT AATGTGAGTT					
3921							
3991	ATGTTGTGTG	GAATTGTGAG	CGGATAACAA	TTTCACACAG	GAAACAGCT'A	TGACCATGAT	TAUGUCAAGU

# Figure 32 D

				KpnI		XhoI	
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4061	GCGCAATTAA	CCCTCACTAA	AGGGAACAAA	AGCTGGGTAC	CGGGCCCCCC	CTCGAGGTCA	TTCATATGCT
4131	TGAGAAGAGA	GTCGGGATAG	TCCAAAATAA	AACAAAGGTA	AGATTACCTG	GTCAAAAGTG	AAAACATCAG
4201	TTAAAAGGTG	GTATAAGTAA	AATATCGGTA	ATAAAAGGTG	GCCCAAAGTG	AAATTTACTC	TTTTCTACTA
4271	TTATAAAAAT	TGAGGATGTT	TTGTCGGTAC	TTTGATACGT	CATTTTTGTA	TGAATTGGTT	TTTAAGTTTA
4341	TTCGCGATTT	GGAAATGCAT	ATCTGTATTT	GAGTCGGTTT	TTAAGTTCGT	TGCTTTTGTA	AATACAGAGG
4411	GATTTGTATA	AGAAATATCT	TTAAAAAAACC	CATATGCTAA	TTTGACATAA	TTTTTGAGAA	AAATATATAT
	EcoRI	[					
	~~~~	~~~					
4481	TCAGGCGAAT	TCCACAATGA	ACAATAATAA	GATTAAAATA	GCTTGCCCCC	GTTGCAGCGA	TGGGTATTTT
4551	TTCTAGTAAA	ATAAAAGATA	AACTTAGACT	CAAAACATTT	ACAAAAACAA	CCCCTAAAGT	CCTAAAGCCC
4621	AAAGTGCTAT	GCACGATCCA	TAGCAAGCCC	AGCCCAACCC	AACCCAACCC	AACCCACCCC	AGTGCAGCCA
4691	ACTGGCAAAT	AGTCTCCACC	CCCGGCACTA	TCACCGTGAG	TTGTCCGCAC	CACCGCACGT	CTCGCAGCCA
4761	AAAAAAAAA	AAGAAAGAAA	AAAAAGAAAA	AGAAAAACAG	CAGGTGGGTC	CGGGTCGTGG	GGGCCGGAAA
4831	AGCGAGGAGG	ATCGCGAGCA	GCGACGAGGC	CCGGCCCTCC	CTCCGCTTCC	AAAGAAACGC	CCCCCATCGC
4901	CACTATATAC	ATACCCCCCC	CTCTCCTCCC	ATCCCCCCAA	CCCTACCACC	ACCACCACCA	CCACCTCCTC
4971	CCCCCTCGCT	GCCGGACGAC	GAGCTCCTCC	CCCCTCCCCC	TCCGCCGCCG	CCGGTAACCA	CCCCGCCCCT
5041	CTCCTCTTTC	TTTCTCCGTT	TTTTTTTCG	TCTCGGTCTC	GATCTTTGGC	CTTGGTAGTT	TGGGTGGGCG
5111	AGAGCGGCTT	CGTCGCCCAG	ATCGGTGCGC	GGGAGGGGCG	GGATCTCGCG	GCTGGCGTCT	CCGGGCGTGA
	Bar	nHI			BglII		
	~~.	~~~~			~~~~~		
5181	GTCGGCCCGG	ATCCTCGCGG	GGAATGGGGC	TCTCGGATGT	AGATCTTCTT	TCTTTCTTCT	TTTTGTGGTA
5251	GAATTTGAAT	CCCTCAGCAT	TGTTCATCGG	TAGTTTTTCT	TTTCATGATT	TGTGACAAAT	GCAGCCTCGT
5321	GCGGAGCTTT	TTTGTAGC					

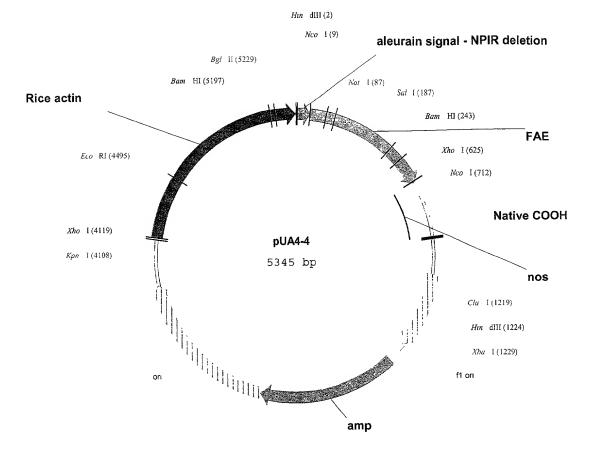


Figure 33 A

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911

981

1051

1121

#### Figure 33 B

NcoI

HindI	ΙI
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M A H A R V L L L A L A V L A T A A V A V AAGCTTACCA TGGCCCACGC CCGCGTCCTC CTCCTGGCGC TCGCCGTGCT GGCCACGGCC GCCGTCGCCG NotI

. ASSRAA ASTO GISEDL YSRL VEM. TCGCCTCCTC CCGCGCGGCC GCCTCCACGC AGGGCATCTC CGAAGACCTC TACAGCCGTT TAGTCGAAAT 71 SalI

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-ATISQAAYAD LCN IPST IIK GEK GGCCACTATC TCCCAAGCTG CCTACGCCGA CCTGTGCAAC ATTCCGTCGA CTATTATCAA GGGAGAGAAA 141 BamHI

I Y N S Q T D I N G W I L R D D S S K E I I T V ATTTACAATT CTCAAACTGA CATTAACGGA TGGATCCTCC GCGACGACAG CAGCAAAGAA ATAATCACCG 211 FRG TGS DTNL QLD TNY TLTP FDT. TCTTCCGTGG CACTGGTAGT GATACGAATC TACAACTCGA TACTAACTAC ACCCTCACGC CTTTCGACAC 281 · L P Q C N G C E V H G G Y Y I G W V S V Q D Q CCTACCACAA TGCAACGGTT GTGAAGTACA CGGTGGATAT TATATTGGAT GGGTCTCCGT CCAGGACCAA VESLVKQQVSQYPDYALTVTGHXL GTCGAGTCGC TTGTCAAACA GCAGGTTAGC CAGTATCCGG ACTACGCGCT GACCGTGACC GGCCACKCCC · G A S L A A L T A A Q L S A T Y D N I R L Y T · TCGGCGCCTC CCTGGCGGCA CTCACTGCCG CCCAGCTGTC TGCGACATAC GACAACATCC GCCTGTACAC 491

F G E P R S G N Q A F A S Y M N D A F Q A S S CTTCGGCGAA CCGCGCAGCG GCAATCAGGC CTTCGCGTCG TACATGAACG ATGCCTTCCA AGCCTCGAGC PDTTQYFRVTHANDGIPNLPPVEQ CCAGATACGA CGCAGTATTT CCGGGTCACT CATGCCAACG ACGGCATCCC AAACCTGCCC CCGGTGGAGC

GYAHGGVEYWSVDPYSAQNTFVC. AGGGGTACGC CCATGGCGGT GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG T G D E V O C C E A Q G G Q G V N N A H T T Y CACTGGGGAT GAAGTGCAGT GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT FGMTSGACTW \* TTTGGGATGA CGAGCGGAGC CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT AATTAACATG TAATGCATGA CGTTATTTAT GAGATGGGTT TTTATGATTA GAGTCCCGCA ATTATACATT TAATACGCGA TAGAAAACAA AATATAGCGC GCAAACTAGG ATAAATTATC HindIII

#### XbaI ClaI

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GCGCGCGTG TCATCTATGT TACTAGATCG ATAAGCTTCT AGAGCGGCCG GTGGAGCTCC AATTCGCCCT 1191 ATAGTGAGTC GTATTACGCG CGCTCACTGG CCGTCGTTTT ACAACGTCGT GACTGGGAAA ACCCTGGCGT 1261 TACCCAACTT AATCGCCTTG CAGCACATCC CCCTTTCGCC AGCTGGCGTA ATAGCGAAGA GGCCCGCACC 1331 GATCGCCCTT CCCAACAGTT GCGCAGCCTG AATGGCGAAT GGGACGCGCC CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT TGCCAGCGCC CTAGCGCCCG CTCCTTTCGC 1471 TTTCTTCCCT TCCTTTCTCG CCACGTTCGC CGGCTTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTTA 1541 GGGTTCCGAT TTAGTGCTTT ACGGCACCTC GACCCCAAAA AACTTGATTA GGGTGATGGT TCACGTAGTG 1611 1681 GGCCATCGCC CTGATAGACG GTTTTTCGCC CTTTGACGTT GGAGTCCACG TTCTTTAATA GTGGACTCTT 1751 GTTCCAAACT GGAACAACAC TCAACCCTAT CTCGGTCTAT TCTTTTGATT TATAAGGGAT TTTGCCGATT TCGGCCTATT GGTTAAAAAA TGAGCTGATT TAACAAAAAT TTAACGCGAA TTTTAACAAA ATATTAACGC TTACAATTTA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCCTATTT GTTTATTTTT CTAAATACAT 1961 TCAAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA Figure 33 C

|                                                                                                                      | mas ams mmas '                                                                                                                                                            | ACATTTCCGT                                                                                                                                                                                 | amaaaaaamma                                                                                                                                                                                | மாப்பட்டுள்ளன்க                                                                                                                                                                  | መረረረረረ እጥጥጥ                                                                                    | <b>ጥር ሶርጥጥር ሶጥር</b>                                                                      | ᡎᡎᡎᡎᡎ᠘ᢕᡎᢕ᠘                                                                                                                                                                                                     |
|----------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 2031                                                                                                                 | TGAGTATTCA                                                                                                                                                                | CTGGTGAAAG                                                                                                                                                                                 | GICGCCCIIA                                                                                                                                                                                 | TICCCITIII                                                                                                                                                                       | TGCGGCATII                                                                                     | CACTCCCTTA                                                                               | CATCGAACTG                                                                                                                                                                                                     |
| 2101                                                                                                                 | CCCAGAAACG                                                                                                                                                                | GCGGTAAGAT                                                                                                                                                                                 | COMMON CR                                                                                                                                                                                  | TURAGAT CAG                                                                                                                                                                      | A A CA A COUNTY                                                                                | TCCN NTCNTC                                                                              | A CCA CTTTTA                                                                                                                                                                                                   |
| 2171                                                                                                                 | GATCTCAACA                                                                                                                                                                | ATGTGGCGCG                                                                                                                                                                                 | CCTTGAGAGI                                                                                                                                                                                 | TITCGCCCCG                                                                                                                                                                       | AAGAACGIII                                                                                     | CAACTCCTTC                                                                               | CCCCCATACA                                                                                                                                                                                                     |
| 2241                                                                                                                 | AAGTTCTGCT                                                                                                                                                                | ATGTGGCGCG                                                                                                                                                                                 | GTATTATCCC                                                                                                                                                                                 | GTATTGACGC                                                                                                                                                                       | CGGGCAAGAG                                                                                     | TTT CCC TTCC                                                                             | CATCACACTA                                                                                                                                                                                                     |
| 2311                                                                                                                 | CTATTCTCAG                                                                                                                                                                | AATGACTTGG                                                                                                                                                                                 | TIGAGIACIC                                                                                                                                                                                 | ACCAGTCACA                                                                                                                                                                       | GAAAAGCAIC                                                                                     | CEER CEECEC                                                                              | ACARCAGIA                                                                                                                                                                                                      |
| 2381                                                                                                                 | AGAGAATTAT                                                                                                                                                                | GCAGTGCTGC                                                                                                                                                                                 | CATAACCATG                                                                                                                                                                                 | AGTGATAACA                                                                                                                                                                       | CTGCGGCCAA                                                                                     | ACTICITIES                                                                               | ACAACGAICG                                                                                                                                                                                                     |
| 2451                                                                                                                 | GAGGACCGAA                                                                                                                                                                | GGAGCTAACC                                                                                                                                                                                 | GCTTTTTTGC                                                                                                                                                                                 | ACAACATGGG                                                                                                                                                                       | GGATCATGTA                                                                                     | ACTOGCCTTG                                                                               | ATCGITGGGA                                                                                                                                                                                                     |
| 2521                                                                                                                 | ACCGGAGCTG                                                                                                                                                                | AATGAAGCCA                                                                                                                                                                                 | TACCAAACGA                                                                                                                                                                                 | CGAGCGTGAC                                                                                                                                                                       | ACCACGATGC                                                                                     | CTGTAGCAAT                                                                               | GGCAACAACG                                                                                                                                                                                                     |
| 2591                                                                                                                 | TTGCGCAAAC                                                                                                                                                                | TATTAACTGG                                                                                                                                                                                 | CGAACTACTT                                                                                                                                                                                 | ACTCTAGCTT                                                                                                                                                                       | CCCGGCAACA                                                                                     | ATTAATAGAC                                                                               | TGGATGGAGG                                                                                                                                                                                                     |
| 2661                                                                                                                 | CGGATAAAGT                                                                                                                                                                | TGCAGGACCA                                                                                                                                                                                 | CTTCTGCGCT                                                                                                                                                                                 | CGGCCCTTCC                                                                                                                                                                       | GGCTGGCTGG                                                                                     | TTTATTGCTG                                                                               | ATAAATCTGG                                                                                                                                                                                                     |
| 2731                                                                                                                 | AGCCGGTGAG                                                                                                                                                                | CGTGGGTCTC                                                                                                                                                                                 | GCGGTATCAT                                                                                                                                                                                 | TGCAGCACTG                                                                                                                                                                       | GGGCCAGATG                                                                                     | GTAAGCCCTC                                                                               | CCGTATCGTA                                                                                                                                                                                                     |
| 2801                                                                                                                 | GTTATCTACA                                                                                                                                                                | CGACGGGGAG                                                                                                                                                                                 | TCAGGCAACT                                                                                                                                                                                 | ATGGATGAAC                                                                                                                                                                       | GAAATAGACA                                                                                     | GATCGCTGAG                                                                               | ATAGGTGCCT                                                                                                                                                                                                     |
| 2871                                                                                                                 | CACTGATTAA                                                                                                                                                                | GCATTGGTAA                                                                                                                                                                                 | CTGTCAGACC                                                                                                                                                                                 | AAGTTTACTC                                                                                                                                                                       | ATATATACTT                                                                                     | TAGATTGATT                                                                               | TAAAACTTCA                                                                                                                                                                                                     |
| 2941                                                                                                                 | TTTTTAATTT                                                                                                                                                                | AAAAGGATCT                                                                                                                                                                                 | AGGTGAAGAT                                                                                                                                                                                 | CCTTTTTGAT                                                                                                                                                                       | AATCTCATGA                                                                                     | CCAAAATCCC                                                                               | TTAACGTGAG                                                                                                                                                                                                     |
| 3011                                                                                                                 | TTTTCGTTCC                                                                                                                                                                | ACTGAGCGTC                                                                                                                                                                                 | AGACCCCGTA                                                                                                                                                                                 | GAAAAGATCA                                                                                                                                                                       | AAGGATCTTC                                                                                     | TTGAGATCCT                                                                               | TTTTTTCTGC                                                                                                                                                                                                     |
| 3081                                                                                                                 | GCGTAATCTG                                                                                                                                                                | CTGCTTGCAA                                                                                                                                                                                 | ACAAAAAAAC                                                                                                                                                                                 | CACCGCTACC                                                                                                                                                                       | AGCGGTGGTT                                                                                     | TGTTTGCCGG                                                                               | ATCAAGAGCT                                                                                                                                                                                                     |
| 3151                                                                                                                 | ACCAACTCTT                                                                                                                                                                | TTTCCGAAGG                                                                                                                                                                                 | TAACTGGCTT                                                                                                                                                                                 | CAGCAGAGCG                                                                                                                                                                       | CAGATACCAA                                                                                     | ATACTGTCCT                                                                               | TCTAGTGTAG                                                                                                                                                                                                     |
| 3221                                                                                                                 | CCGTAGTTAG                                                                                                                                                                | GCCACCACTT                                                                                                                                                                                 | CAAGAACTCT                                                                                                                                                                                 | GTAGCACCGC                                                                                                                                                                       | CTACATACCT                                                                                     | CGCTCTGCTA                                                                               | ATCCTGTTAC                                                                                                                                                                                                     |
| 3291                                                                                                                 | CAGTGGCTGC                                                                                                                                                                | TGCCAGTGGC                                                                                                                                                                                 | ${\tt GATAAGTCGT}$                                                                                                                                                                         | GTCTTACCGG                                                                                                                                                                       | GTTGGACTCA                                                                                     | AGACGATAGT                                                                               | TACCGGATAA                                                                                                                                                                                                     |
| 3361                                                                                                                 | GGCGCAGCGG                                                                                                                                                                | TCGGGCTGAA                                                                                                                                                                                 | CGGGGGGTTC                                                                                                                                                                                 | GTGCACACAG                                                                                                                                                                       | CCCAGCTTGG                                                                                     | AGCGAACGAC                                                                               | CTACACCGAA                                                                                                                                                                                                     |
| 3431                                                                                                                 | CTGAGATACC                                                                                                                                                                | TACAGCGTGA                                                                                                                                                                                 | GCTATGAGAA                                                                                                                                                                                 | AGCGCCACGC                                                                                                                                                                       | TTCCCGAAGG                                                                                     | GAGAAAGGCG                                                                               | GACAGGTATC                                                                                                                                                                                                     |
| 3501                                                                                                                 | CGGTAAGCGG                                                                                                                                                                | CAGGGTCGGA                                                                                                                                                                                 | ACAGGAGAGC                                                                                                                                                                                 | GCACGAGGGA                                                                                                                                                                       | GCTTCCAGGG                                                                                     | GGAAACGCCT                                                                               | GGTATCTTTA                                                                                                                                                                                                     |
| 3571                                                                                                                 | TAGTCCTGTC                                                                                                                                                                | GGGTTTCGCC                                                                                                                                                                                 | ACCTCTGACT                                                                                                                                                                                 | TGAGCGTCGA                                                                                                                                                                       | TTTTTGTGAT                                                                                     | GCTCGTCAGG                                                                               | GGGGCGGAGC                                                                                                                                                                                                     |
| 3641                                                                                                                 | CTATGGAAAA                                                                                                                                                                | ACGCCAGCAA                                                                                                                                                                                 | CGCGGCCTTT                                                                                                                                                                                 | TTACGGTTCC                                                                                                                                                                       | TGGCCTTTTG                                                                                     | CTGGCCTTTT                                                                               | GCTCACATGT                                                                                                                                                                                                     |
| 3711                                                                                                                 | TCTTTCCTGC                                                                                                                                                                | GTTATCCCCT                                                                                                                                                                                 | GATTCTGTGG                                                                                                                                                                                 | ATAACCGTAT                                                                                                                                                                       | TACCGCCTTT                                                                                     | GAGTGAGCTG                                                                               | ATACCGCTCG                                                                                                                                                                                                     |
| 3781                                                                                                                 | CCGCAGCCGA                                                                                                                                                                | ACGACCGAGC                                                                                                                                                                                 | GCAGCGAGTC                                                                                                                                                                                 | AGTGAGCGAG                                                                                                                                                                       | GAAGCGGAAG                                                                                     | AGCGCCCAAT                                                                               | ACGCAAACCG                                                                                                                                                                                                     |
| 3851                                                                                                                 | CCTCTCCCCG                                                                                                                                                                | CGCGTTGGCC                                                                                                                                                                                 | GATTCATTAA                                                                                                                                                                                 | TGCAGCTGGC                                                                                                                                                                       | ACGACAGGTT                                                                                     | TCCCGACTGG                                                                               | AAAGCGGGCA                                                                                                                                                                                                     |
| 3921                                                                                                                 | GTGAGCGCAA                                                                                                                                                                | CGCAATTAAT                                                                                                                                                                                 | GTGAGTTAGC                                                                                                                                                                                 | TCACTCATTA                                                                                                                                                                       | GGCACCCCAG                                                                                     | GCTTTACACT                                                                               | TTATGCTTCC                                                                                                                                                                                                     |
| 3991                                                                                                                 | GGCTCGTATG                                                                                                                                                                | TTGTGTGGAA                                                                                                                                                                                 | TTGTGAGCGG                                                                                                                                                                                 | ATAACAATTT                                                                                                                                                                       | CACACAGGAA                                                                                     | ACAGCTATGA                                                                               | CCATGATTAC                                                                                                                                                                                                     |
|                                                                                                                      |                                                                                                                                                                           |                                                                                                                                                                                            |                                                                                                                                                                                            |                                                                                                                                                                                  | KpnI                                                                                           | Xho                                                                                      |                                                                                                                                                                                                                |
|                                                                                                                      |                                                                                                                                                                           |                                                                                                                                                                                            |                                                                                                                                                                                            |                                                                                                                                                                                  | ~~~~~                                                                                          | ~~~                                                                                      |                                                                                                                                                                                                                |
|                                                                                                                      |                                                                                                                                                                           |                                                                                                                                                                                            |                                                                                                                                                                                            | CAACAAAACC                                                                                                                                                                       | TCCCTACCC                                                                                      | acacacacama                                                                              |                                                                                                                                                                                                                |
| 4061                                                                                                                 | GCCAAGCGCG                                                                                                                                                                | CAATTAACCC                                                                                                                                                                                 | TCACTAAAGG                                                                                                                                                                                 | CHACHANGC                                                                                                                                                                        | IGGGIACCGG                                                                                     | GCCCCCCCCC                                                                               | GAGGTCATTC                                                                                                                                                                                                     |
| 4061<br>4131                                                                                                         | GCCAAGCGCG<br>ATATGCTTGA                                                                                                                                                  | GAAGAGAGTC                                                                                                                                                                                 | GGGATAGTCC                                                                                                                                                                                 | AAAATAAAAC                                                                                                                                                                       | AAAGGTAAGA                                                                                     | TTACCTGGTC                                                                               | AAAAGTGAAA                                                                                                                                                                                                     |
| 4131                                                                                                                 | ATATGCTTGA<br>ACATCAGTTA                                                                                                                                                  | GAAGAGAGTC<br>AAAGGTGGTA                                                                                                                                                                   | GGGATAGTCC<br>TAAGTAAAAT                                                                                                                                                                   | AAAATAAAAC<br>ATCGGTAATA                                                                                                                                                         | AAAGGTAAGA<br>AAAGGTGGCC                                                                       | TTACCTGGTC<br>CAAAGTGAAA                                                                 | AAAAGTGAAA<br>TTTACTCTTT                                                                                                                                                                                       |
|                                                                                                                      | ATATGCTTGA<br>ACATCAGTTA<br>TCTACTATTA                                                                                                                                    | GAAGAGAGTC<br>AAAGGTGGTA<br>TAAAAATTGA                                                                                                                                                     | GGGATAGTCC<br>TAAGTAAAAT<br>GGATGTTTTG                                                                                                                                                     | AAAATAAAAC<br>ATCGGTAATA<br>TCGGTACTTT                                                                                                                                           | AAAGGTAAGA<br>AAAGGTGGCC<br>GATACGTCAT                                                         | TTACCTGGTC<br>CAAAGTGAAA<br>TTTTGTATGA                                                   | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT                                                                                                                                                                         |
| 4131<br>4201<br>4271                                                                                                 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC                                                                                                                               | GAAGAGAGTC<br>AAAGGTGGTA<br>TAAAAATTGA<br>GCGATTTGGA                                                                                                                                       | GGGATAGTCC<br>TAAGTAAAAT<br>GGATGTTTTG<br>AATGCATATC                                                                                                                                       | AAAATAAAAC<br>ATCGGTAATA<br>TCGGTACTTT<br>TGTATTTGAG                                                                                                                             | AAAGGTAAGA<br>AAAGGTGGCC<br>GATACGTCAT<br>TCGGTTTTTA                                           | TTACCTGGTC<br>CAAAGTGAAA<br>TTTTGTATGA<br>AGTTCGTTGC                                     | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT                                                                                                                                                           |
| 4131<br>4201<br>4271<br>4341                                                                                         | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC                                                                                                                               | GAAGAGAGTC<br>AAAGGTGGTA<br>TAAAAATTGA<br>GCGATTTGGA                                                                                                                                       | GGGATAGTCC<br>TAAGTAAAAT<br>GGATGTTTTG<br>AATGCATATC                                                                                                                                       | AAAATAAAAC<br>ATCGGTAATA<br>TCGGTACTTT<br>TGTATTTGAG                                                                                                                             | AAAGGTAAGA<br>AAAGGTGGCC<br>GATACGTCAT<br>TCGGTTTTTA                                           | TTACCTGGTC<br>CAAAGTGAAA<br>TTTTGTATGA<br>AGTTCGTTGC                                     | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT                                                                                                                                                           |
| 4131<br>4201<br>4271                                                                                                 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC                                                                                                                               | GAAGAGAGTC<br>AAAGGTGGTA<br>TAAAAATTGA                                                                                                                                                     | GGGATAGTCC<br>TAAGTAAAAT<br>GGATGTTTTG<br>AATGCATATC                                                                                                                                       | AAAATAAAAC<br>ATCGGTAATA<br>TCGGTACTTT<br>TGTATTTGAG                                                                                                                             | AAAGGTAAGA<br>AAAGGTGGCC<br>GATACGTCAT<br>TCGGTTTTTA                                           | TTACCTGGTC<br>CAAAGTGAAA<br>TTTTGTATGA<br>AGTTCGTTGC                                     | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT                                                                                                                                                           |
| 4131<br>4201<br>4271<br>4341                                                                                         | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC ACAGAGGGAT                                                                                                                    | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI                                                                                                                               | GGGATAGTCC<br>TAAGTAAAAT<br>GGATGTTTTG<br>AATGCATATC<br>AATATCTTTA                                                                                                                         | AAAATAAAAC<br>ATCGGTAATA<br>TCGGTACTTT<br>TGTATTTGAG<br>AAAAACCCAT                                                                                                               | AAAGGTAAGA<br>AAAGGTGGCC<br>GATACGTCAT<br>TCGGTTTTTA<br>ATGCTAATTT                             | TTACCTGGTC<br>CAAAGTGAAA<br>TTTTGTATGA<br>AGTTCGTTGC<br>GACATAATTT                       | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA                                                                                                                                             |
| 4131<br>4201<br>4271<br>4341<br>4411                                                                                 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC ACAGAGGGAT                                                                                                                    | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI                                                                                                                               | GGGATAGTCC<br>TAAGTAAAAT<br>GGATGTTTTG<br>AATGCATATC<br>AATATCTTTA                                                                                                                         | AAAATAAAAC<br>ATCGGTAATA<br>TCGGTACTTT<br>TGTATTTGAG<br>AAAAACCCAT                                                                                                               | AAAGGTAAGA<br>AAAGGTGGCC<br>GATACGTCAT<br>TCGGTTTTTA<br>ATGCTAATTT                             | TTACCTGGTC<br>CAAAGTGAAA<br>TTTTGTATGA<br>AGTTCGTTGC<br>GACATAATTT                       | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA                                                                                                                                             |
| 4131<br>4201<br>4271<br>4341<br>4411                                                                                 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC ACAGAGGGAT TATATATTCA                                                                                                         | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI                                                                                                                               | GGGATAGTCC<br>TAAGTAAAAT<br>GGATGTTTTG<br>AATGCATATC<br>AATATCTTTA<br>ACAATGAACA                                                                                                           | AAAATAAAAC ATCGGTAATA TCGGTACTTT TGTATTTGAG AAAAACCCAT ATAATAAGAT                                                                                                                | AAAGGTAAGA<br>AAAGGTGGCC<br>GATACGTCAT<br>TCGGTTTTTA<br>ATGCTAATTT<br>TAAAATAGCT               | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT TGCCCCCGTT                        | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG                                                                                                                               |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551                                                                 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC ACAGAGGGAT TATATATTCA GTATTTTTTC                                                                                              | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI GGCGAATTCC                                                                                                                    | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA ACAATGAACA AAAGATAAAC                                                                                                               | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA                                                                                                              | AAAGGTAAGA<br>AAAGGTGGCC<br>GATACGTCAT<br>TCGGTTTTTA<br>ATGCTAATTT<br>TAAAATAGCT<br>AACATTTACA | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT TGCCCCCGTT AAAACAACCC             | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT                                                                                                                 |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621                                                         | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC ACAGAGGGAT  TATATATTCA GTATTTTTCC AAAGCCCAAA                                                                                  | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI GGCGAATTCC TAGTAAAATA GTGCTATGCA                                                                                              | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA ACAATGAACA AAAGATAAAC CGATCCATAG                                                                                                    | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC                                                                                                   | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT TGCCCCCGTT AAAACAACCC CCAACCCAAC  | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT                                                                                                   |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691                                                 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC ACAGAGGGAT  TATATATTCA GTATTTTTTC AAAGCCCAAA GCAGCCAACT                                                                       | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI GGCGAATTCC TAGTAAAATA GTGCTATGCA                                                                                              | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCCC                                                                                        | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA                                                                                        | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT TGCCCCCGTT AAAACAACCC CCAACCCAAC  | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC                                                                                     |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761                                         | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC ACAGAGGGAT  TATATATTCA GTATTTTTCC AAAGCCCAAA GCAGCCAAAA                                                                       | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI GGCGAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT                                                                                   | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCCC AAAGAAAAAA                                                                             | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA                                                                             | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC<br>GTCGTGGGGG                                                                       |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831                                 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC ACAGAGGGAT  TATATATTCA GTATTTTTC AAAGCCCAAA GCAGCCAAAA CCGGAAAAAGC                                                            | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI GGCGAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT AAAAAAAAAGG                                                                       | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCC AAAGAAAAAA GCGAGCAGCG                                                                   | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA ACGAGGCCCG                                                                  | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC<br>GTCGTGGGGG<br>GAAACGCCCC                                                         |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901                         | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTC ACAGAGGGAT  TATATATTCA GTATTTTTC AAAGCCCAAA GCAGCCAAAA CCGGAAAAGC                                                             | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI GGCGAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT AAAAAAAAAG GAGGAGGATC                                                             | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCC AAAGAAAAAA GCGAGCAGCG CCCCCCCCTC                                                        | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA ACGAGGCCCG TCCTCCCATC                                                       | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC<br>GTCGTGGGGG<br>GAAACGCCCC<br>ACCACCACCA                                           |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971                 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTCA ACAGAGGGAT  TATATATTCA GTATTTTTTC AAAGCCCAAA GCAGCCAACT GCAGCCAAAA CCGGAAAAGC CCATCGCCAC                                     | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI TAGTAAAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT AAAAAAAAAG GAGGAGGATC TATATACATA                                                | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCC AAAGAAAAAA GCGAGCAGCG CCCCCCCTC GGACGACGAG                                              | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA ACGAGGCCCG TCCTCCCATC                                                       | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC<br>GTCGTGGGGG<br>GAAACGCCCC<br>ACCACCACCA<br>GTAACCACCC                             |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971<br>5041         | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTCA ACAGAGGGAT  TATATATTCA GTATTTTTCC AAAGCCCAAA GCAGCCAACT GCAGCCAAAA CCGGAAAAGC CCATCGCCAC CCTCCTCCCCC                         | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI TAGTAAAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT AAAAAAAAAG GAGGAGGATC TATATACATA CCTCGCTGCC                                     | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCC AAAGAAAAAA GCGAGCAGCG CCCCCCCTC GGACGACGAG CTCCGTTTTT                                   | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA ACGAGGCCCG TCCTCCCATC CTCCTCCCCC TTTTTCGTCT                                 | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC<br>GTCGTGGGGG<br>GAAACGCCCC<br>ACCACCACCA<br>GTAACCACCC<br>GGTAGTTTGG               |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971                 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTCA ACAGAGGGAT  TATATATTCA GTATTTTTCC AAAGCCCAAA GCAGCCAACT GCAGCCAAAA CCGGAAAAGC CCATCGCCAC CCTCCTCCCCC                         | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI TAGTAAAATA GGCGAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT AAAAAAAAG GAGGAGGATC TATATACATA CCTCGCTGCC CTCTTTCTTT GCGGCTTCGT       | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCC AAAGAAAAAA GCGAGCAGCG CCCCCCCTC GGACGACGAG CTCCGTTTTT CGCCCAGATC                        | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA ACGAGGCCCG TCCTCCCATC CTCCTCCCCC TTTTTCGTCT                                 | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC<br>GTCGTGGGGG<br>GAAACGCCCC<br>ACCACCACCA<br>GTAACCACCC                             |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971<br>5041         | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTCA ACAGAGGGAT  TATATATTCA GTATTTTTCC AAAGCCCAAA GCAGCCAACT GCAGCCAAAA CCGGAAAAGC CCATCGCCAC CCTCCTCCCCC                         | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI TAGTAAAATA GGCGAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT AAAAAAAAG GAGGAGGATC TATATACATA CCTCGCTGCC CTCTTTCTTT GCGGCTTCGT BamhI | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCC AAAGAAAAAA GCGAGCAGCG CCCCCCCTC GGACGACGAG CTCCGTTTTT CGCCCAGATC                        | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA ACGAGGCCCG TCCTCCCATC CTCCTCCCCC TTTTTCGTCT                                 | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC<br>GTCGTGGGGG<br>GAAACGCCCC<br>ACCACCACCA<br>GTAACCACCC<br>GGTAGTTTGG               |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971<br>5041<br>5111 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTCA ACAGAGGGAT  TATATATTCA GTATTTTTCA AAAGCCCAAA GCAGCCAACT GCAGCCAAAA CCGGAAAAGC CCATCGCCAC CCTCCTCCCC GTGGGCGAGA               | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI TAGTAAAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT AAAAAAAAAG GAGGAGGATC TATATACATA CCTCGCTGCC CTCTTTCTTT GCGGCTTCGT BamHI         | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCCC AAAGAAAAAA GCGAGCAGCG CCCCCCCTC GGACGACGAG CTCCGTTTTT CGCCCAGATC                       | AAAATAAAAC ATCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA ACGAGGCCCG TCCTCCCATC CTCCTCCCCC TTTTTCGTCT GGTGCGCGGG                      | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC<br>GTCGTGGGGG<br>GAAACGCCCC<br>ACCACCACCA<br>GTAACCACCC<br>GGTAGTTTGG<br>GGCGTCTCCG |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971<br>5041<br>5111 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTCA ACAGAGGGAT  TATATATTCA GTATTTTTCA AAAGCCCAAA GCAGCCAACT GCAGCCAAAA CCGGAAAAGC CCATCGCCAC CGCCCTCTCC GTGGGCGAGA               | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI TAGTAAAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT AAAAAAAAAG GAGGAGGATC TATATACATA CCTCGCTGCC CTCTTTCTTT GCGGCTTCGT BamHI         | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCC AAAGAAAAAA GCGAGCAGCG CCCCCCCTC GGACGACGAG CTCCGTTTTT CGCCCAGATC                        | AAAATAAAAC ATCGGTAATA TCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA ACGAGGCCCG TCCTCCCATC CTCCTCCCCC TTTTTCGTCT GGTGCGCGGG ATGGGGCCGG | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA TTTACTCTTT ATTGGTTTTT TTTTGTAAAT TTGAGAAAAA  GCAGCGATGG CTAAAGTCCT CCACCCCAGT CGCACGTCTC GTCGTGGGGG GAAACGCCCC ACCACCACCA GTAACCACCC GGTAGTTTGG GGCGTCTCCG TTCTCTTTT                                |
| 4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971<br>5041<br>5111 | ATATGCTTGA ACATCAGTTA TCTACTATTA AAGTTTATTCA ACAGAGGGAT  TATATATTCA GTATTTTTCA AAAGCCCAAAA GCAGCCAAAA CCGGAAAAAGC CCATCGCCAC CGCCCTCTCC GTGGGCGAGA GGCGTGAGAC TGTGGTAGAAA | GAAGAGAGTC AAAGGTGGTA TAAAAATTGA GCGATTTGGA TTGTATAAGA ECORI TAGTAAAATTCC TAGTAAAATA GTGCTATGCA GGCAAATAGT AAAAAAAAAG GAGGAGGATC TATATACATA CCTCGCTGCC CTCTTTCTTT GCGGCTTCGT BamHI         | GGGATAGTCC TAAGTAAAAT GGATGTTTTG AATGCATATC AATATCTTTA  ACAATGAACA AAAGATAAAC CGATCCATAG CTCCACCCC AAAGAAAAAA GCGAGCAGCG CCCCCCCTC GGACGACGAG CTCCGTTTTT CGCCCAGATC  CTCGCGGGGA TCAGCATTGT | AAAATAAAAC ATCGGTAATA TCGGTACTTT TGTATTTGAG AAAAACCCAT  ATAATAAGAT TTAGACTCAA CAAGCCCAGC GGCACTATCA AAGAAAAAGA ACGAGGCCCG TCCTCCCATC CTCCTCCCCC TTTTTCGTCT GGTGCGCGGG ATGGGGCCGG | AAAGGTAAGA AAAGGTGGCC GATACGTCAT TCGGTTTTTA ATGCTAATTT  TAAAATAGCT AACATTTACA CCAACCCAAC       | TTACCTGGTC CAAAGTGAAA TTTTGTATGA AGTTCGTTGC GACATAATTT  TGCCCCCGTT AAAACAACCC CCAACCCAAC | AAAAGTGAAA<br>TTTACTCTTT<br>ATTGGTTTTT<br>TTTTGTAAAT<br>TTGAGAAAAA<br>GCAGCGATGG<br>CTAAAGTCCT<br>CCACCCCAGT<br>CGCACGTCTC<br>GTCGTGGGGG<br>GAAACGCCCC<br>ACCACCACCA<br>GTAACCACCC<br>GGTAGTTTGG<br>GGCGTCTCCG |

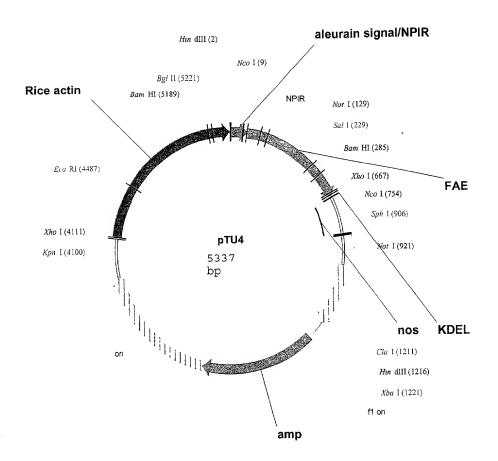


Figure 34 A

1261

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1401

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1611

#### Figure 34 B

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|      | HindIII                                                                                                                            |
|------|------------------------------------------------------------------------------------------------------------------------------------|
|      | ~~~~                                                                                                                               |
| 1    | M A H A R V L L L A L A V L A T A A V A V AAGCTTACCA TGGCCCACGC CCGCGTCCTC CTCCTGGCGC TCGCCGTGCT GGCCACGGCC GCCGTCGCCG Not I       |
|      | . ASSSSF ADSN PIR PVT DRAA AST.                                                                                                    |
| 71   | TCGCCTCCTC CTCCTCCTTC GCCGACTCCA ACCCGATCCG GCCCGTCACC GACCGCGCGG CCGCCTCCAC  O G I S E D L Y S R L V E M A T I S Q A A Y A        |
| 141  | GCAGGGCATC TCCGAAGACC TCTACAGCCG TTTAGTCGAA ATGGCCACTA TCTCCCAAGC TGCCTACGCC<br>Sali                                               |
|      | ~~~~~                                                                                                                              |
| 211  | D L C N I P S T I I K G E K I Y N S Q T D I N G GACCTGTGCA ACATTCCGTC GACTATTATC AAGGGAGAGA AAATTTACAA TTCTCAAACT GACATTAACG BamHI |
|      | . WIL RDD SSKE IIT V F R G T G S D T N                                                                                             |
| 281  | GATGGATCCT CCGCGACGAC AGCAGCAAAG AAATAATCAC CGTCTTCCGT GGCACTGGTA GTGATACGAA . I. O I. D T N Y T L T P F D T L P Q C N G C E V     |
| 351  | TCTACAACTC GATACTAACT ACACCCTCAC GCCTTTCGAC ACCCTACCAC AATGCAACGG TTGTGAAGTA<br>H G G Y Y I G W V S V Q D Q V E S L V K Q Q V S    |
| 421  | CACGGTGGAT ATTATATTGG ATGGGTCTCC GTCCAGGACC AAGTCGAGTC GCTTGTCAAA CAGCAGGTTA . Q Y P D Y A L T V T G H X L G A S L A A L T A       |
| 491  | GCCAGTATCC GGACTACGCG CTGACCGTGA CCGGCCACKC CCTCGGCGCC TCCCTGGCGG CACTCACTGC  · A Q L S A T Y D N I R L Y T F G E P R S G N Q      |
| 561  | CGCCCAGCTG TCTGCGACAT ACGACAACAT CCGCCTGTAC ACCTTCGGCG AACCGCGCAG CGGCAATCAG  XhoI                                                 |
| 631  | A F A S Y M N D A F Q A S S P D T T Q Y F R V T GCCTTCGCGT CGTACATGAA CGATGCCTTC CAAGCCTCGA GCCCAGATAC GACGCAGTAT TTCCGGGTCA  NCOI |
|      | . HANDGIPNLPPVE QGYAHGG VEY                                                                                                        |
| 701  | CTCATGCCAA CGACGGCATC CCAAACCTGC CCCCGGTGGA GCAGGGGTAC GCCCATGGCG GTGTAGAGTA . W S V D P Y S A O N T F V C T G D E V Q C C E       |
| 771  | CTGGAGCGTT GATCCTTACA GCGCCCAGAA CACATTTGTC TGCACTGGGG ATGAAGTGCA GTGCTGTGAG SphI                                                  |
|      | AOGG QGV N N A H T T Y F G M T S G A C T W                                                                                         |
| 841  | GCCCAGGGCG GACAGGGTGT GAATAATGCG CACACGACTT ATTTTGGGAT GACGAGCGGC GCATGCACCT Not!                                                  |
|      | · P V A A A E P L K D E L *                                                                                                        |
| 911  | GGCCGGTCGC GGCCGCGAA CCACTGAAGG ATGAGCTGTA AAGAAGCAGA TCGTTCAAAC ATTTGGCAAT                                                        |
| 981  | AAAGTTTCTT AAGATTGAAT CCTGTTGCCG GTCTTGCGAT GATTATCATA TAATTTCTGT TGAATTACGT                                                       |
| 1051 | TAAGCATGTA ATAATTAACA TGTAATGCAT GACGTTATTT ATGAGATGGG TTTTTATGAT TAGAGTCCCG                                                       |
| 1121 | CAATTATACA TTTAATACGC GATAGAAAAC AAAATATAGC GCGCAAACTA GGATAAATTA TCGCGCGCGG<br>HindIII                                            |
|      | ClaI XbaI                                                                                                                          |
| 1191 | TGTCATCTAT GTTACTAGAT CGATAAGCTT CTAGAGCGGC CGGTGGAGCT CCAATTCGCC CTATAGTGAG                                                       |

TCGTATTACG CGCGCTCACT GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC

TTAATCGCCT TGCAGCACAT CCCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATCGCCC

TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGGACGCG CCCTGTAGCG GCGCATTAAG CGCGGCGGGT

GTGGTGGTTA CGCGCAGCGT GACCGCTACA CTTGCCAGCG CCCTAGCGCC CGCTCCTTTC GCTTTCTTCC

CTTCCTTTCT CGCCACGTTC GCCGGCTTTC CCCGTCAAGC TCTAAATCGG GGGCTCCCTT TAGGGTTCCG

ATTTAGTGCT TTACGGCACC TCGACCCCAA AAAACTTGAT TAGGGTGATG GTTCACGTAG TGGGCCATCG

# Figure 34 C

| 1681 | CCCTGATAGA | CGGTTTTTCG | CCCTTTGACG | TTGGAGTCCA | CGTTCTTTAA  | TAGTGGACTC | TTGTTCCAAA |
|------|------------|------------|------------|------------|-------------|------------|------------|
| 1751 |            |            | ATCTCGGTCT |            |             |            |            |
| 1821 | TTGGTTAAAA | AATGAGCTGA | TTTAACAAAA | ATTTAACGCG | AATTTTAACA  | AAATATTAAC | GCTTACAATT |
| 1891 |            |            | AATGTGCGCG |            |             |            |            |
| 1961 |            |            | AACCCTGATA |            |             |            |            |
| 2031 | CAACATTTCC | GTGTCGCCCT | TATTCCCTTT | TTTGCGGCAT | TTTGCCTTCC  | TGTTTTTGCT | CACCCAGAAA |
| 2101 |            |            | GCTGAAGATC |            |             |            |            |
| 2171 |            |            | GTTTTCGCCC |            |             |            |            |
| 2241 |            |            | CCGTATTGAC |            |             |            |            |
| 2311 |            |            | TCACCAGTCA |            |             |            |            |
|      |            |            | TGAGTGATAA |            |             |            |            |
| 2381 | AIGCAGIGCI | CCCATAACCA | GCACAACATG | CACIGOGGC  | TAACTIACTIC | TCATCCTTCC | CAACCCCACC |
| 2451 |            |            | GACGAGCGTG |            |             |            |            |
| 2521 |            |            | TTACTCTAGC |            |             |            |            |
| 2591 |            |            | CTCGGCCCTT |            |             |            |            |
| 2661 |            |            | ATTGCAGCAC |            |             |            |            |
| 2731 |            |            |            |            |             |            |            |
| 2801 |            |            | CTATGGATGA |            |             |            |            |
| 2871 |            |            | CCAAGTTTAC |            |             |            |            |
| 2941 |            |            | ATCCTTTTTG |            |             |            |            |
| 3011 |            |            | TAGAAAAGAT |            |             |            |            |
| 3081 |            |            | ACCACCGCTA |            |             |            |            |
| 3151 |            |            | TTCAGCAGAG |            |             |            |            |
| 3221 |            |            | CTGTAGCACC |            |             |            |            |
| 3291 |            |            | GTGTCTTACC |            |             |            |            |
| 3361 |            |            | TCGTGCACAC |            |             |            |            |
| 3431 |            |            | AAAGCGCCAC |            |             |            |            |
| 3501 |            |            | GCGCACGAGG |            |             |            |            |
| 3571 | TCGGGTTTCG | CCACCTCTGA | CTTGAGCGTC | GATTTTTGTG | ATGCTCGTCA  | GGGGGGCGGA | GCCTATGGAA |
| 3641 |            |            | TTTTACGGTT |            |             |            |            |
| 3711 |            |            | GGATAACCGT |            |             |            |            |
| 3781 |            |            | TCAGTGAGCG |            |             |            |            |
| 3851 |            |            | AATGCAGCTG |            |             |            |            |
| 3921 |            |            | GCTCACTCAT |            |             |            |            |
| 3991 | TGTTGTGTGG | AATTGTGAGC | GGATAACAAT | TTCACACAGG | AAACAGCTAT  | GACCATGATT | ACGCCAAGCG |
|      |            |            |            | KpnI       | Σ           | KhoI       |            |
|      |            |            |            | ~~~~~      | -           | ~~~~       |            |
| 4061 |            |            | GGGAACAAAA |            |             |            |            |
| 4131 |            |            | CCAAAATAAA |            |             |            |            |
| 4201 |            |            | ATATCGGTAA |            |             |            |            |
| 4271 |            |            | TGTCGGTACT |            |             |            |            |
| 4341 |            |            | TCTGTATTTG |            |             |            |            |
| 4411 | ATTTGTATAA | GAAATATCTT | TAAAAAACCC | ATATGCTAAT | TTGACATAAT  | TTTTGAGAAA | AATATATATT |
|      | EcoRI      |            |            |            |             |            |            |
|      | ~~~~       |            |            |            |             |            | ~~~~       |
| 4481 |            |            | CAATAATAAG |            |             |            |            |
| 4551 |            |            | ACTTAGACTC |            |             |            |            |
| 4621 |            | -          | AGCAAGCCCA |            |             |            |            |
| 4691 |            |            | CCGGCACTAT |            |             |            |            |
| 4761 |            |            | AAAAGAAAAA |            |             |            |            |
| 4831 |            |            | CGACGAGGCC |            |             |            |            |
| 4901 |            |            | TCTCCTCCCA |            |             |            |            |
| 4971 |            |            | AGCTCCTCCC |            |             |            |            |
| 5041 | TCCTCTTTCT | TTCTCCGTTT | TTTTTTTCGT | CTCGGTCTCG | ATCTTTGGCC  | TTGGTAGTTT | GGGTGGGCGA |
| 5111 | GAGCGGCTTC | GTCGCCCAGA | TCGGTGCGCG |            |             | CTGGCGTCTC | CGGGCGTGAG |
| ,    | Bami       | HI         |            | B          | glII        |            |            |
| •    |            | ~~~        |            |            | ~~~~        |            |            |
| 5181 |            |            |            |            |             |            | TTTGTGGTAG |
| 5251 | AATTTGAATC | CCTCAGCATT | GTTCATCGGT | AGTTTTTCTT | TTCATGATTT  | GTGACAAATG | CAGCCTCGTG |
| 5321 | CGGAGCTTTT | TTGTAGC    |            |            |             |            |            |
|      |            |            |            |            |             |            |            |

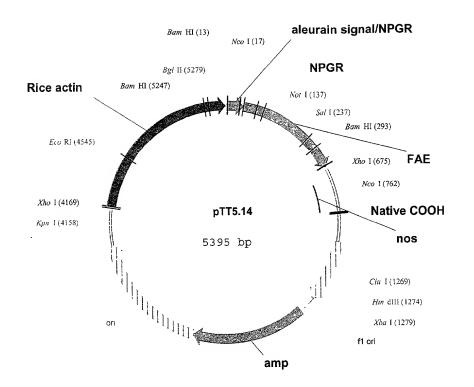


Figure 35 A

### Figure 35 B

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| BamH: | Ι |
|-------|---|
|       |   |

|                                                                                  | Deliase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|----------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                                                                                  | M A H A R V L L A L A V L A T A A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| 1                                                                                | CCTGACGCCG AGGATCCATG GCCCACGCCC GCGTCCTCCT CCTGGCGCTC GCCGTGCTGG CCACGGCCGC Noti                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| 71                                                                               | . V A V A S S S S F A D S N P G R P V T D R A A CGTCGCCGTC GCCTCCTCCT CCTCCTTCGC CGACTCCAAC CCGGGCCGGC CCGTCACCGA CCGCGCGGCC NotI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| 141                                                                              | A S T Q G I S E D L Y S R L V E M A T I S Q A A GCCTCCACGC AGGGCATCTC CGAAGACCTC TACAGCCGTT TAGTCGAAAT GGCCACTATC TCCCAAGCTG  SalI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 211                                                                              | . Y A D L C N I P S T I I K G E K I Y N S Q T D CCTACGCCGA CCTGTGCAAC ATTCCGTCGA CTATTATCAA GGGAGAGAAA ATTTACAATT CTCAAACTGA BamHI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 281                                                                              | · I N G W I L R D D S S K E I I T V F R G T G S CATTAACGGA TGGATCCTCC GCGACGACAG CAGCAAAGAA ATAATCACCG TCTTCCGTGG CACTGGTAGT D T N L O L D T N Y T L T P F D T L P Q C N G C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 351                                                                              | GATACGAATC TACAACTCGA TACTAACTAC ACCCTCACGC CTTTCGACAC CCTACCACAA TGCAACGGTT  · E V H G G Y Y I G W V S V Q D Q V E S L V K Q                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| 421                                                                              | GTGAAGTACA CGGTGGATAT TATATTGGAT GGGTCTCCGT CCAGGACCAA GTCGAGTCGC TTGTCAAACA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 491                                                                              | GCAGGTTAGC CAGTATCCGG ACTACGCGCT GACCGTGACC GGCCACKCCC TCGGCGCCTC CCTGGCGGCACAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 561                                                                              | CTCACTGCCG CCCAGCTGTC TGCGACATAC GACAACATCC GCCTGTACAC CTTCGGCGAA CCGCGCAGCG XhoI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|                                                                                  | . NOAFAS Y M N D A F Q A S S P D T T Q Y F                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 631                                                                              | GCAATCAGGC CTTCGCGTCG TACATGAACG ATGCCTTCCA AGCCTCGAGC CCAGATACGA CGCAGTATTT Ncol                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|                                                                                  | . R V T H A N D G I P N L P P V E Q G Y A H G G                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 701                                                                              | RVTHANDGIPNLPPVEQGIAHGGCCCCCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| 701                                                                              | CCGGGTCACT CATGCCAACG ACGCCATCCC AAACCTGCCC CCGGTGGAGC AGGGGTACGC CCATGGCGGT V F Y W S V D P Y S A Q N T F V C T G D E V Q C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 771                                                                              | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|                                                                                  | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT . C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 771                                                                              | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGGGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 771<br>841                                                                       | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGGGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 771<br>841<br>911<br>981<br>1051                                                 | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 771<br>841<br>911<br>981<br>1051                                                 | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT AATTAACATT                                                                                                                                                                                                                                                                                                                                                                                                               |
| 771<br>841<br>911<br>981<br>1051                                                 | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT AATTAACATG TAATGCATGA CGTTATTTAT GAGATGGGTT TTTATGATTA GAGTCCCGCA ATTATACATT TAATACGCGA TAGAAAACAA AATATAGCGC GCAAACTAGG ATAAAATTATC GCGCGCGGTG TCATCTATGT                                                                                                                                                                                                                                                               |
| 771<br>841<br>911<br>981<br>1051                                                 | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGATACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT AATTAACATG TAATGCATGA CGTTATTTAT GAGATGGGTT TTTATGATTA GAGTCCCGCA ATTATACATT TAATACGCGA TAGAAAACAA AATATAGCGC GCAAACTAGG ATAAATTATC GCGCGCGGTG TCATCTATGT                                                                                                                                                                                                                                                               |
| 771<br>841<br>911<br>981<br>1051                                                 | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT AATTAACATG TAATGCATGA CGTTATTTAT GAGATGGGTT TTTATGATTA GAGTCCCGCA ATTATACATT TAATACGCGA TAGAAAACAA AATATAGCGC GCAAACTAGG ATAAATTATC GCGCGCGGTG TCATCTATGT HindIII  CCACCACACACACACACACACACACACACACACAC                                                                                                                                                                                                                    |
| 771<br>841<br>911<br>981<br>1051<br>1121<br>1191                                 | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGGGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT TAATGACATG TAATGCATGA CGTTATTTAT GAGATGGGTT TTTATGATTA GAGTCCCGCA ATTATACATT TAATACACGC TAGAAAACAA AATATAGCGC GCAAACTAGG ATAAATTATC GCGCGCGGTG TCATCTATGT Hindlii  Clai Xbai  TACTAGATCG ATAAGCTTCT AGAGCGGCCG GTGGAGCTCC AATTCGCCCT ATAGTGAGTC GTATTACGCG                                                                                                                                                                |
| 771<br>841<br>911<br>981<br>1051<br>1121<br>1191                                 | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT AATTAACATG TAATGCATGA CGTTATTTAT GAGATGGGTT TTTATGATTA GAGTCCCGCA ATTATACATT TAATACGCGA TAGAAAACAA AATATAGCGC GCAAACTAGG ATAAATTATC GCGCGCGGTG TCATCTATGT  Hindlii  Clai Xbai  TACTAGATCG ATAAGCTTCT AGAGCGGCCG GTGGAGCTCC AATTCGCCCT ATAGTGAGTC GTATTACGCG CGCTCACTGG CCGTCGTTTT ACAACGTCGT GACTGGGAAA ACCCTGGCGT TACCCCAACTT AATCGCCTTG                                                                                |
| 771<br>841<br>911<br>981<br>1051<br>1121<br>1191<br>1261<br>1331<br>1401         | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT AATTAACATG TAATGCATGA CGTTATTTAT GAGATGGGTT TTTATGATTA GAGTCCCGCA ATTATACATT TAATACGCGA TAGAAAACAA AATATAGCGC GCAAACTAGG ATAAATTATC GCGCGCGGTG TCATCTATGT  Hindlii  Clai Xbai  TACTAGATCG ATAAGCTTCT AGAGCGGCCG GTGGAGCTCC AATTCGCCCT ATAGTGAGTC GTATTACGCG CGCTCACTGG CCGTCGTTTT ACAACGTCGT GACTGGGAAAA ACCCTGGCGT TACCCAACTT AATCGCCTTG CAGCACATCC CCCTTTCGCC AGCTGGCGTA ATAGCGAAGA GGCCCCGCACC GATCGCCCTT CCCCAACAGTT |
| 771<br>841<br>911<br>981<br>1051<br>1121<br>1191<br>1261<br>1331<br>1401<br>1471 | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TATACATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT TAATGCAGGA TAGAAAACAA AATATAGCGC GCAAACTAGG ATAAATTATC GCGCGCGCGGTG TCATCTATGT  HINDLI  Clal Xbal  TACTAGATCG ATAAGCTTCT AGAGCGGCCG GTGGAGCTCC AATTCGCCCT ATAGTGAGTC GTATTACGCG CGCTCACTGG CCGTCGTTTT ACAACGTCGT GACTGGGAAAA ACCCTGGCGT TACCCAACTT AATCGCCTTG CAGCACATCC CCCTTTCGCC AGCTGGCGTA ATAGCGAAGA GGCCCGCACC GATCGCCCTT CCCAACAGTT GCGCAGCCTG AATGGCGAAT GGGACGCCC CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG    |
| 771<br>841<br>911<br>981<br>1051<br>1121<br>1191<br>1261<br>1331<br>1401         | V E Y W S V D P Y S A Q N T F V C T G D E V Q C GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG CACTGGGGAT GAAGTGCAGT  C E A Q G G Q G V N N A H T T Y F G M T S G A GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT TTTGGGATGA CGAGCGGAGC  C T W *  CTGTACATGG TGATCAGTCA TTTCAGCCTC CCCGAGTGTA CCAGGAAAGA TGGATGTCCT GGAGAGGGGG CCGCGTAACC ACTGAAGGAT GAGCTGTAAA GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT AATTAACATG TAATGCATGA CGTTATTTAT GAGATGGGTT TTTATGATTA GAGTCCCGCA ATTATACATT TAATACGCGA TAGAAAACAA AATATAGCGC GCAAACTAGG ATAAATTATC GCGCGCGGTG TCATCTATGT  Hindlii  Clai Xbai  TACTAGATCG ATAAGCTTCT AGAGCGGCCG GTGGAGCTCC AATTCGCCCT ATAGTGAGTC GTATTACGCG CGCTCACTGG CCGTCGTTTT ACAACGTCGT GACTGGGAAAA ACCCTGGCGT TACCCAACTT AATCGCCTTG CAGCACATCC CCCTTTCGCC AGCTGGCGTA ATAGCGAAGA GGCCCCGCACC GATCGCCCTT CCCCAACAGTT |

1751 GTTTTCGCC CTTTGACGTT GGAGTCCACG TTCTTTAATA GTGGACTCTT GTTCCAAACT GGAACAACAC

## Figure <u>35</u>C

|         |             | ·                   |                  |                                         |                          | maaaaama mm  | 0.000000000000000000000000000000000000 |
|---------|-------------|---------------------|------------------|-----------------------------------------|--------------------------|--------------|----------------------------------------|
| 1821    | TCAACCCTAT  | CTCGGTCTAT          | TCTTTTGATT       | TATAAGGGAT                              | TTTGCCGATT               | TCGGCCTATT   | GGTTAAAAAA                             |
| 1891    | TGAGCTGATT  | TAACAAAAAT          | TTAACGCGAA       | TTTTAACAAA                              | ATATTAACGC               | TTACAATTTA   | GGTGGCAC'I'I'                          |
| 1961    | TTCGGGGAAA  | TGTGCGCGGA          | ACCCCTATTT       | GTTTATTTTT                              | CTAAATACAT               | TCAAATATGT   | ATCCGCTCAT                             |
| 2031    | GAGACAATAA  | CCCTGATAAA          | TGCTTCAATA       | ATATTGAAAA                              | AGGAAGAGTA               | TGAGTATTCA   | ACATTTCCGT                             |
| 2101    | GTCGCCCTTA  | TTCCCTTTTT          | TGCGGCATTT       | TGCCTTCCTG                              | TTTTTGCTCA               | CCCAGAAACG   | CTGGTGAAAG                             |
|         | TANA ACATIC | TGAAGATCAG          | TTCCCTCCAC       | CACTCCCTTA                              | CATCGAACTG               | GATCTCAACA   | GCGGTAAGAT                             |
| 2171    | TAAAAGA TGC | TTTCGCCCCG          | TIGOTOCAC        | THE | A CCA CTTTTA             | AACTTCTCTCCT | ATCTCCCCC                              |
| 2241    | CCTTGAGAGT  | TTTCGCCCCG          | AAGAACGIII       | CLAATGATG                               | AGCACITIA                | AAGIICIGCI   | A TOTA CETTOO                          |
| 2311    | GTATTATCCC  | GTATTGACGC          | CGGGCAAGAG       | CAACTCGGTC                              | GCCGCATACA               | CTATTCTCAG   | AAIGACIIGG                             |
| 2381    | TTGAGTACTC  | ACCAGTCACA          | GAAAAGCATC       | TTACGGATGG                              | CATGACAGTA               | AGAGAATTAT   | GCAGTGCTGC                             |
| 2451    | CATAACCATG  | AGTGATAACA          | CTGCGGCCAA       | CTTACTTCTG                              | ACAACGATCG               | GAGGACCGAA   | GGAGCTAACC                             |
| 2521    | GCTTTTTTGC  | ACAACATGGG          | GGATCATGTA       | ACTCGCCTTG                              | ATCGTTGGGA               | ACCGGAGCTG   | AATGAAGCCA                             |
| 2591    | TACCAAACGA  | CGAGCGTGAC          | ACCACGATGC       | CTGTAGCAAT                              | GGCAACAACG               | TTGCGCAAAC   | TATTAACTGG                             |
| 2661    | CGAACTACTT  | ACTCTAGCTT          | CCCGGCAACA       | ATTAATAGAC                              | TGGATGGAGG               | CGGATAAAGT   | TGCAGGACCA                             |
| 2731    | CTTCTCCCCCT | CGGCCCTTCC          | GGCTGGCTGG       | TTTATTGCTG                              | ATAAATCTGG               | AGCCGGTGAG   | CGTGGGTCTC                             |
|         | CITCIOCCCI  | TGCAGCACTG          | CCCCCACATC       | GTA AGCCCTC                             | CCGTATCGTA               | GTTATCTACA   | CGACGGGGAG                             |
| 2801    | GCGGIAICAI  | ATGGATGAAC          | CANAMACACA       | CATCCCTCAC                              | ATACCTCCCT               | CACTGATTAA   | CCATTCCTAA                             |
| 2871    | TCAGGCAACT  | ATGGATGAAC          | GAAATAGACA       | GAICGCIGAG                              | MIAGGIGCCI               | CACIGATIAA   | AAAACCATCT                             |
| 2941    | CTGTCAGACC  | AAGTTTACTC          | ATATATACTT       | TAGATTGATT                              | TAAAACTICA               | TITITAATTI   | AAAAGGATCI                             |
| 3011    | AGGTGAAGAT  | CCTTTTTGAT          | AATCTCATGA       | CCAAAATCCC                              | TTAACGTGAG               | TTTTCGTTCC   | ACTGAGCGTC                             |
| 3081    | AGACCCCGTA  | GAAAAGATCA          | AAGGATCTTC       | TTGAGATCCT                              | TTTTTTCTGC               | GCGTAATCTG   | CTGCTTGCAA                             |
| 3151    | ACAAAAAAAC  | CACCGCTACC          | AGCGGTGGTT       | TGTTTGCCGG                              | ATCAAGAGCT               | ACCAACTCTT   | TTTCCGAAGG                             |
| 3221    | TAACTGGCTT  | CAGCAGAGCG          | CAGATACCAA       | ATACTGTCCT                              | TCTAGTGTAG               | CCGTAGTTAG   | GCCACCACTT                             |
| 3291    | CAAGAACTCT  | GTAGCACCGC          | CTACATACCT       | CGCTCTGCTA                              | ATCCTGTTAC               | CAGTGGCTGC   | TGCCAGTGGC                             |
| 3361    | CATAACTCCT  | GTCTTACCGG          | GTTGGACTCA       | AGACGATAGT                              | TACCGGATAA               | GGCGCAGCGG   | TCGGGCTGAA                             |
| 3431    | CCCCCCCCTTC | GTGCACACAG          | CCCAGCTTGG       | AGCGAACGAC                              | CTACACCGAA               | CTGAGATACC   | TACAGCGTGA                             |
|         | COOOGGGGGGG | AGCGCCACGC          | TTCCCCAAGG       | CACAAACCCC                              | GACAGGTATC               | CGGTAAGCGG   | CAGGGTCGGA                             |
| 3501    | GCIAIGAGAA  | GCACGAGGGA          | COMMOGRACO       | CCAAAACCCC                              | CCTATCTTTA               | TACTCCTCTC   | CCCTTTCCCC                             |
| 3571    | ACAGGAGAGC  | TGAGCGTCGA          | GCTTCCAGGG       | GGAAACGCCI                              | CCCCCCCCCCC              | CTATCCIAIA   | ACCCCACCAA                             |
| 3641    | ACCTCTGACT  | TGAGCGTCGA          | TTTTTGTGAT       | GCTCGTCAGG                              | COUCUCACO                | CIAIGGAAAA   | ACGCCAGCAA                             |
| 3711    | CGCGGCCTTT  | TTACGGTTCC          | TGGCCTTTTG       | CTGGCCTTTT                              | GCTCACATGT               | TCTTTCCTGC   | GITATCCCCI                             |
| 3781    | GATTCTGTGG  | ATAACCGTAT          | TACCGCCTTT       | GAGTGAGCTG                              | ATACCGCTCG               | CCGCAGCCGA   | ACGACCGAGC                             |
| 3851    | GCAGCGAGTC  | AGTGAGCGAG          | GAAGCGGAAG       | AGCGCCCAAT                              | ACGCAAACCG               | CCTCTCCCCG   | CGCGTTGGCC                             |
| 3921    | GATTCATTAA  | TGCAGCTGGC          | ACGACAGGTT       | TCCCGACTGG                              | AAAGCGGGCA               | GTGAGCGCAA   | CGCAATTAAT                             |
| 3991    | GTGAGTTAGC  | TCACTCATTA          | GGCACCCCAG       | GCTTTACACT                              | TTATGCTTCC               | GGCTCGTATG   | TTGTGTGGAA                             |
| 4061    | TTGTGAGCGG  | ATAACAATTT          | CACACAGGAA       | ACAGCTATGA                              | CCATGATTAC               | GCCAAGCGCG   | CAATTAACCC                             |
|         |             |                     | KpnI             | Xho                                     |                          |              |                                        |
|         |             |                     | ~~~~~            | ~~~                                     | ~~~                      |              |                                        |
| 4131    | maxamxxxac  | GAACAAAAGC          |                  | CCCCCCCCTC                              | $G\Delta GGTC\Delta TTC$ | ATATGCTTGA   | GAAGAGAGTC                             |
|         | CACTAAAGG   | AAAATAAAAC          | AAACCTAACA       | THE CONCOUNT                            | AAAAGTGAAA               | ACATCACTTA   | AAAGGTGGTA                             |
| 4201    | GGGATAGICC  | ATCGGTAATA          | AAAGGIAAGA       | CARACTIGGIC                             | WWWYG I GWYY             | TOTACTATTA   | TANANATTCA                             |
| 4271    | TAAGTAAAAT  | ATCGGTAATA          | AAAGGTGGCC       | CAAAGIGAAA                              | TITACICITI               | 1CIACIAIIA   | CCCAMMMCCA                             |
| 4341    | GGATGTTTTG  | TCGGTACTTT          | GATACGTCAT       | TTTTGTATGA                              | ATTGGTTTTT               | AAGTTTATTC   | GCGATTIGGA                             |
| 4411    | AATGCATATC  | TGTATTTGAG          | TCGGTTTTTA       | AGTTCGTTGC                              | TTTTGTAAAT               | ACAGAGGGAT   |                                        |
|         |             |                     |                  |                                         |                          |              | EcoRI                                  |
|         |             |                     |                  |                                         |                          |              | ~                                      |
| 4481    |             | AAAAACCCAT          |                  |                                         |                          |              |                                        |
| 4551    | ACAATGAACA  | ATAATAAGAT          | TAAAATAGCT       | TGCCCCCGTT                              | GCAGCGATGG               | GTATTTTTC    | TAGTAAAATA                             |
| 4621    |             | TTAGACTCAA          |                  |                                         |                          |              |                                        |
| 4691    |             | CAAGCCCAGC          |                  |                                         |                          |              |                                        |
| 4761    | CECCA CCCCC | CAAGCCCAGC          | CCCTCACTTC       | TCCGCACCAC                              | CGCACGTCTC               | GCAGCCAAAA   | AAAAAAAAAG                             |
|         | CICCACCCC   | AAGAAAAAGA          | Z Z Z Z CZ CCZ C | CTCCCCCCCCC                             | CUCACCICIC               | CCCGAAAACC   | CACCACCATC                             |
| 4831    | AAAGAAAAA   | AAGAAAAAGA          | AAAACAGCAG       | GIGGGICCGG                              | GICGIGGGG                | CCGGAAAAGC   | TAUCAGAIC                              |
| 4901    | GCGAGCAGCG  | ACGAGGCCCG          | GCCCTCCCTC       | CGCTTCCAAA                              | GAAACGCCCC               | CCATCGCCAC   | TATATACATA                             |
| 4971    | CCCCCCCTC   | TCCTCCCATC          | CCCCCAACCC       | TACCACCACC                              | ACCACCACCA               | CCTCCTCCCC   | CCTCGCTGCC                             |
| 5041    | GGACGACGAG  | CTCCTCCCC           | CTCCCCCTCC       | GCCGCCGCCG                              | GTAACCACCC               | CGCCCCTCTC   | CTCTTTCTTT                             |
| 5111    | CTCCGTTTTT  | TTTTTCGTCT          | CGGTCTCGAT       | CTTTGGCCTT                              | GGTAGTTTGG               | GTGGGCGAGA   | GCGGCTTCGT                             |
|         |             |                     |                  |                                         |                          |              | ${\tt BamHI}$                          |
| 5181    | CGCCCAGATC  | GGTGCGCGG           | AGGGGCGGA        | TCTCGCGGCT                              | GGCGTCTCCG               | GGCGTGAGTC   | GGCCCGGATC                             |
| + - O - | BamHI       |                     | Bql              |                                         |                          |              |                                        |
|         | ~           |                     | _                | ~~~~                                    |                          |              |                                        |
| E2E1    |             | א תוכובור הייים ייי |                  |                                         |                          | ТСТССТАСА    | TTTGAATCCC                             |
| 5251    |             |                     |                  |                                         |                          |              | GAGCTTTTTT                             |
| 5321    |             | TCATCGGTAG          | · IIIIICTTTT     | CAIGAIIIGI                              | UNCAMA I GCA             | CCICGIGCG    | CAGCIIIIII                             |
| 5391    | GTAGC       |                     |                  |                                         |                          |              |                                        |
|         |             |                     |                  |                                         |                          |              |                                        |

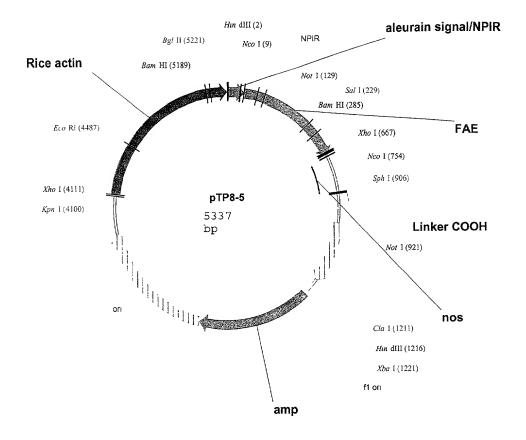


Figure 36\_A

1471

#### Figure <u>3</u>B

NcoI ~~~~~

| Hind | Ι | Ι | Ι |
|------|---|---|---|
|------|---|---|---|

|       | ~~~~                                                                                                                         |
|-------|------------------------------------------------------------------------------------------------------------------------------|
|       | M A H A R V L L L A L A V L A T A A V A V                                                                                    |
| 1     | AAGCTTACCA TGGCCCACGC CCGCGTCCTC CTCCTGGCGC TCGCCGTGCT GGCCACGGCC GCCGTCGCCG                                                 |
| _     | NotI                                                                                                                         |
|       | ~~~~~                                                                                                                        |
|       | . ASSSSFADSN PIR PVT DRAA AST                                                                                                |
| 71    | TCGCCTCCTC CTCCTCCTTC GCCGACTCCA ACCCGATCCG GCCCGTCACC GACCGCGCGG CCGCCTCCAC                                                 |
| , _   | OGISEDLYSRLVEMATISQAAYA                                                                                                      |
| 1 4 1 | GCAGGGCATC TCCGAAGACC TCTACAGCCG TTTAGTCGAA ATGGCCACTA TCTCCCAAGC TGCCTACGCC                                                 |
| 141   | Sali                                                                                                                         |
|       | 5411                                                                                                                         |
|       |                                                                                                                              |
| 011   | D L C N I P S T I I K G E K I Y N S Q T D I N G GACCTGTGCA ACATTCCGTC GACTATTATC AAGGGAGAGA AAATTTACAA TTCTCAAACT GACATTAACG |
| 211   |                                                                                                                              |
|       | BamHI                                                                                                                        |
|       | · W I L R D D S S K E I I T V F R G T G S D T N                                                                              |
|       | . W I L R D D S S K E I I T V F R G T G S D T N GATGGATCCT CCGCGACGAC AGCAGCAAAG AAATAATCAC CGTCTTCCGT GGCACTGGTA GTGATACGAA |
| 281   |                                                                                                                              |
|       |                                                                                                                              |
| 351   | TCTACAACTC GATACTAACT ACACCCTCAC GCCTTTCGAC ACCCTACCAC AATGCAACGG TTGTGAAGTA H G G Y Y I G W V S V Q D Q V E S L V K Q Q V S |
|       |                                                                                                                              |
| 421   | CACGGTGGAT ATTATATTGG ATGGGTCTCC GTCCAGGACC AAGTCGAGTC GCTTGTCAAA CAGCAGGTTA                                                 |
|       | . Q Y P D Y A L T V T G H X L G A S L A A L T A                                                                              |
| 491   | GCCAGTATCC GGACTACGCG CTGACCGTGA CCGGCCACKC CCTCGGCGCC TCCCTGGCGG CACTCACTGC                                                 |
|       | · A Q L S A T Y D N I R L Y T F G E P R S G N Q                                                                              |
| 561   | CGCCCAGCTG TCTGCGACAT ACGACAACAT CCGCCTGTAC ACCTTCGGCG AACCGCGCAG CGGCAATCAG                                                 |
|       | XhoI                                                                                                                         |
|       |                                                                                                                              |
|       | A F A S Y M N D A F Q A S S P D T T Q Y F R V T                                                                              |
| 631   | GCCTTCGCGT CGTACATGAA CGATGCCTTC CAAGCCTCGA GCCCAGATAC GACGCAGTAT TTCCGGGTCA                                                 |
|       | NCO1                                                                                                                         |
|       |                                                                                                                              |
|       | . H A N D G I P N L P P V E Q G Y A H G G V E Y CTCATGCCAA CGACGGCATC CCAAACCTGC CCCCGGTGGA GCAGGGGTAC GCCCATGGCG GTGTAGAGTA |
| 701   |                                                                                                                              |
|       | · W S V D P Y S A Q N T F V C T G D E V Q C C E CTGGAGCGTT GATCCTTACA GCGCCCAGAA CACATTTGTC TGCACTGGGG ATGAAGTGCA GTGCTGTGAG |
| 771   | CIGGAGCGIT GATCCITACA GCGCCCAGAA CACAIIIGIC IGCACIGGGG AIGAAGIGCA GIGCIGIGAG SphI                                            |
|       | Spiil ~~~~                                                                                                                   |
|       | AQGGQGVNNA HTTY FGM TSG ACT V                                                                                                |
| 0.4.5 | GCCCAGGGCG GACAGGGTGT GAATAATGCG CACACGACTT ATTTTGGGAT GACGAGCGGC GCATGCACCT                                                 |
| 841   |                                                                                                                              |
|       | NotI                                                                                                                         |
|       |                                                                                                                              |
| 0 7 7 | · P V A A A *  GGCCGGTCGC GGCCGCGTAA CCACTGAAGG ATGAGCTGTA AAGAAGCAGA TCGTTCAAAC ATTTGGCAAT                                  |
| 911   | AAAGTTTCTT AAGATTGAAT CCTGTTGCCG GTCTTGCGAT GATTATCATA TAATTTCTGT TGAATTACGT                                                 |
| 981   | AAAGTTTCTT AAGATTGAAT CCTGTTGCCG GTCTTGCGAT GATTALCATA TAATTCTGT IGAATTACGT                                                  |
| 1051  | TAAGCATGTA ATAATTAACA TGTAATGCAT GACGTTATTT ATGAGATGGG TTTTTATGAT TAGAGTCCCG                                                 |
| 1121  | CAATTATACA TTTAATACGC GATAGAAAAC AAAATATAGC GCGCAAACTA GGATAAATTA TCGCGCGCGG                                                 |
|       | HindIII                                                                                                                      |
|       | ~~~~~                                                                                                                        |
|       | ClaI XbaI                                                                                                                    |
|       | ~~~~~~                                                                                                                       |
| 1191  | TGTCATCTAT GTTACTAGAT CGATAAGCTT CTAGAGCGGC CGGTGGAGCT CCAATTCGCC CTATAGTGAG                                                 |
| 1261  | TCGTATTACG CGCGCTCACT GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC                                                 |
| 1331  | TTAATCGCCT TGCAGCACAT CCCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATCGCCC                                                 |
| 1401  | TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGGACGCG CCCTGTAGCG GCGCATTAAG CGCGGCGGGT                                                 |
| 1471  | GTGGTGGTTA CGCGCAGCGT GACCGCTACA CTTGCCAGCG CCCTAGCGCC CGCTCCTTTC GCTTTCTTCC                                                 |

1541 CTTCCTTTCT CGCCACGTTC GCCGGCTTTC CCCGTCAAGC TCTAAATCGG GGGCTCCCTT TAGGGTTCCG ATTTAGTGCT TTACGGCACC TCGACCCCAA AAAACTTGAT TAGGGTGATG GTTCACGTAG TGGGCCATCG

## Figure <u>36</u>C

|         | GGGEG3 E3 G3   | ааатттта          | CCCEETTC A CC                          | mmaaa amaaa | COMMORRED A   | TA CTCCA AMA     | THE CHARGE A A A      |
|---------|----------------|-------------------|----------------------------------------|-------------|---------------|------------------|-----------------------|
| 1681    |                |                   |                                        |             |               | TAGTGGACTC       |                       |
| 1751    |                |                   |                                        |             |               | ATTTTGCCGA       |                       |
| 1821    |                |                   |                                        |             |               | AAATATTAAC       |                       |
| 1891    | TAGGTGGCAC     | TTTTCGGGGA        | AATGTGCGCG                             | GAACCCCTAT  | TTGTTTATTT    | TTCTAAATAC       | ATTCAAATAT            |
| 1961    |                |                   |                                        |             |               | AAAGGAAGAG       |                       |
| 2031    |                |                   |                                        |             |               | TGTTTTTGCT       |                       |
|         |                |                   |                                        |             |               | TACATCGAAC       |                       |
| 2101    |                |                   |                                        |             |               |                  |                       |
| 2171    |                |                   |                                        |             |               | TGAGCACTTT       |                       |
| 2241    |                |                   |                                        |             |               | TCGCCGCATA       |                       |
| 2311    | AGAATGACTT     | GGTTGAGTAC        | TCACCAGTCA                             | CAGAAAAGCA  | TCTTACGGAT    | GGCATGACAG       | TAAGAGAATT            |
| 2381    |                |                   |                                        |             |               | TGACAACGAT       |                       |
| 2451    | AAGGAGCTAA     | CCGCTTTTTT        | GCACAACATG                             | GGGGATCATG  | TAACTCGCCT    | TGATCGTTGG       | GAACCGGAGC            |
| 2521    | TGAATGAAGC     | CATACCAAAC        | GACGAGCGTG                             | ACACCACGAT  | GCCTGTAGCA    | ATGGCAACAA       | CGTTGCGCAA            |
| 2591    |                |                   |                                        |             |               | ACTGGATGGA       |                       |
| 2661    | CTTCCACCAC     | CACTTCTGCG        | СТССССССТТ                             | СССССТСССТ  | GGTTTATTGC    | TGATAAATCT       | GGAGCCGGTG            |
|         |                |                   |                                        |             |               | TCCCGTATCG       |                       |
| 2731    |                |                   |                                        |             |               | AGATAGGTGC       |                       |
| 2801    |                |                   |                                        |             |               |                  |                       |
| 2871    |                |                   |                                        |             |               | TTTAAAACTT       |                       |
| 2941    |                |                   |                                        |             |               | CCTTAACGTG       |                       |
| 3011    |                |                   |                                        |             |               | CTTTTTTCT        |                       |
| 3081    | TGCTGCTTGC     | AAACAAAAAA        | ACCACCGCTA                             | CCAGCGGTGG  | TTTGTTTGCC    | GGATCAAGAG       | CTACCAACTC            |
| 3151    | TTTTTCCGAA     | GGTAACTGGC        | TTCAGCAGAG                             | CGCAGATACC  | AAATACTGTC    | CTTCTAGTGT       | AGCCGTAGTT            |
| 3221    |                |                   |                                        |             |               | TAATCCTGTT       |                       |
| 3291    |                |                   |                                        |             |               | GTTACCGGAT       |                       |
|         |                |                   |                                        |             |               | ACCTACACCG       |                       |
| 3361    |                |                   |                                        |             |               | CGGACAGGTA       |                       |
| 3431    |                |                   |                                        |             |               |                  |                       |
| 3501    |                |                   |                                        |             |               | CTGGTATCTT       |                       |
| 3571    |                |                   |                                        |             |               | GGGGGGCGGA       |                       |
| 3641    | AAACGCCAGC     | AACGCGGCCT        | TTTTACGGTT                             | CCTGGCCTTT  | TGCTGGCCTT    | TTGCTCACAT       | GTTCTTTCCT            |
| 3711    |                |                   |                                        |             |               | TGATACCGCT       |                       |
| 3781    |                |                   |                                        |             |               | ATACGCAAAC       |                       |
| 3851    | CGCGCGTTGG     | CCGATTCATT        | AATGCAGCTG                             | GCACGACAGG  | TTTCCCGACT    | GGAAAGCGGG       | CAGTGAGCGC            |
| 3921    |                |                   |                                        |             |               | CTTTATGCTT       |                       |
| .3991   |                |                   |                                        |             |               | GACCATGATT       |                       |
| 3,7,5,1 | 101101010      |                   |                                        | KpnI        |               | KhoI             |                       |
|         |                |                   |                                        | ~~~~~       |               | ~~~~             |                       |
| 1061    | GGG7 7 HH7 7 G | COMOR OTTORA      | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ |             |               | TCGAGGTCAT       | ייים אייז ייים מייייי |
| 4061    |                |                   |                                        |             |               |                  |                       |
| 4131    |                |                   |                                        |             |               | TCAAAAGTGA       |                       |
| 4201    | TAAAAGGTGG     | TATAAGTAAA        | ATATCGGTAA                             | TAAAAGGTGG  | CCCAAAGTGA    | AATTTACTCT       | TTTCTACTAT            |
| 4271    |                |                   |                                        |             |               | GAATTGGTTT       |                       |
| 4341    |                |                   |                                        |             |               | GCTTTTGTAA       |                       |
| 4411    | ATTTGTATAA     | GAAATATCTT        | TAAAAAACCC                             | ATATGCTAAT  | TTGACATAAT    | TTTTGAGAAA       | AATATATATT            |
|         | EcoRI          |                   |                                        |             |               |                  |                       |
|         | ~~~~           | ~~                |                                        |             |               |                  |                       |
| 4481    | CACCCCAA $TT$  | ССАСААТСАА        | САДТАДТАДС                             | ΑΤΤΑΑΑΑΤΑ   | CTTGCCCCCG    | TTGCAGCGAT       | GGGTATTTTT            |
| 4551    |                |                   |                                        |             |               | CCCTAAAGTC       |                       |
|         |                |                   |                                        |             |               | ACCCACCCCA       |                       |
| 4621    |                |                   |                                        |             |               |                  |                       |
| 4691    |                |                   |                                        |             |               | ACCGCACGTC       |                       |
| 4761    |                |                   |                                        |             |               | GGGTCGTGGG       |                       |
| 4831    |                |                   |                                        |             |               | AAGAAACGCC       |                       |
| 4901    |                |                   |                                        |             |               | CCACCACCAC       |                       |
| 4971    | CCCCTCGCTG     | CCGGACGACG        | AGCTCCTCCC                             | CCCTCCCCCT  | CCGCCGCCGC    | CGGTAACCAC       | CCCGCCCCTC            |
| 5041    |                |                   |                                        |             |               |                  | GGGTGGGCGA            |
| 5111    |                |                   |                                        |             |               | CTGGCGTCTC       |                       |
| J + - 1 | Bam            |                   | 10010000                               |             | qlII          | 1100001010       | 20000010110           |
|         |                |                   |                                        |             | 9 <b>.</b> 11 |                  |                       |
| -101    |                | ~~~~<br>maamaaaaa | C3 3 ECCCCC                            |             |               | CHITTICATA CITTE | mmmamaama a           |
| 5181    |                |                   |                                        |             |               | CTTTCTTCTT       |                       |
| 5251    |                |                   | GTTCATCGGT                             | AGTTTTTTTTT | TTCATGATTT    | GTGACAAATG       | CAGCCTCGTG            |
| 5321    | CGGAGCTTTT     | TTGTAGC           |                                        |             |               |                  |                       |
|         |                |                   |                                        |             |               |                  |                       |

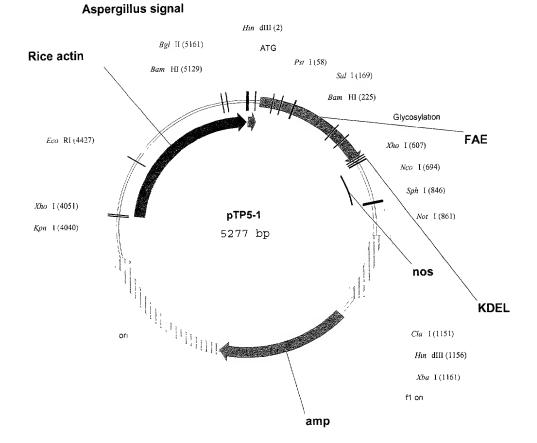


Figure 37 A

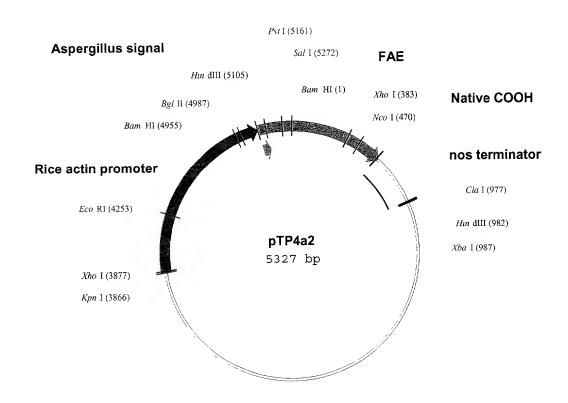
## Figure <u>39</u>B

|      | HindIII PstI                                                                                                                                              |
|------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|
|      | M K O F S A K H V L A V V V T A G H A L                                                                                                                   |
|      | V V X 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1                                                                                                               |
| 1    | AAGCTTAACA TGAAGCAGTT CTCCGCCAAA CACGTCCTCG CAGTTGTGGT GACTGCAGGG CACGCCTTAG $\cdot$ A S T Q G I S E D L Y S R L V E M A T I S Q A                        |
| 71   | . CAGCCTCTAC GCAAGGCATC TCCGAAGACC TCTACAGCCG TTTAGTCGAA ATGGCCACTA TCTCCCAAGC Sali                                                                       |
|      | ~~~~                                                                                                                                                      |
| 141  | · A Y A D L C N I P S T I I K G E K I Y N S Q T TGCCTACGCC GACCTGTGCA ACATTCCGTC GACTATTATC AAGGGAGAGA AAATTTACAA TTCTCAAACT Bamhi                        |
|      | DING WIL RDD S S K E I I T V F R G T G                                                                                                                    |
| 211  | S GACATTAACG GATGGATCCT CCGCGACGAC AGCAGCAAAG AAATAATCAC CGTCTTCCGT GGCACTGGTA . D T N L Q L D T N Y T L T P F D T L P Q C N G                            |
| 281  | . GTGATACGAA TCTACAACTC GATACTAACT ACACCCTCAC GCCTTTCGAC ACCCTACCAC AATGCAACGG                                                                            |
| 201  | C F V H C C V Y T G W V S V O D Q V E S L V K                                                                                                             |
| 351  | TTGTGAAGTA CACGGTGGAT ATTATATTGG ATGGGTCTCC GTCCAGGACC AAGTCGAGTC GCTTGTCAAA QQVSQYPDYALTVT GHXLGA SLA                                                    |
| 421  | A CAGCAGGTTA GCCAGTATCC GGACTACGCG CTGACCGTGA CCGGCCACKC CCTCGGCGCC TCCCTGGCGG $\cdot$ L T A A Q L S A T Y D N I R L Y T F G E P R S                      |
| 491  | . CACTCACTGC CGCCCAGCTG TCTGCGACAT ACGACAACAT CCGCCTGTAC ACCTTCGGCG AACCGCGCAG XhoI                                                                       |
| 561  | · G N Q A F A S Y M N D A F Q A S S P D T T Q Y  CGGCAATCAG GCCTTCGCGT CGTACATGAA CGATGCCTTC CAAGCCTCGA GCCCAGATAC GACGCAGTAT  NCOI                       |
|      | F R V T H A N D G I P N L P P V E Q G Y A H G                                                                                                             |
|      | G.                                                                                                                                                        |
| 631  | TTCCGGGTCA CTCATGCCAA CGACGGCATC CCAAACCTGC CCCCGGTGGA GCAGGGGTAC GCCCATGGCG $\cdot$ V E Y W S V D P Y S A Q N T F V C T G D E V Q                        |
| 701  | GTGTAGAGTA CTGGAGCGTT GATCCTTACA GCGCCCAGAA CACATTTGTC TGCACTGGGG ATGAAGTGCA                                                                              |
| ,01  | .ccr a o g g o g v n n a h t t y f g m t s g                                                                                                              |
| 771  | GTGCTGTGAG GCCCAGGGCG GACAGGGTGT GAATAATGCG CACACGACTT ATTTTGGGAT GACGAGCGGC SphI NotI                                                                    |
|      | ACTWPVAAAEPLKDEL*                                                                                                                                         |
| 841  | GCATGCACCT GGCCGGTCGC GGCCGCGGAA CCACTGAAGG ATGAGCTGTA AAGAAGCAGA TCGTTCAAAC                                                                              |
| 911  | ATTTGGCAAT AAAGTTTCTT AAGATTGAAT CCTGTTGCCG GTCTTGCGAT GATTATCATA TAATTTCTGT                                                                              |
| 981  | TGAATTACGT TAAGCATGTA ATAATTAACA TGTAATGCAT GACGTTATTT ATGAGATGGG TTTTTATGAT TAGAGTCCCG CAATTATACA TTTAATACGC GATAGAAAAC AAAATATAGC GCGCAAACTA GGATAAATTA |
| 1051 | HindIII                                                                                                                                                   |
|      | ClaI XbaI                                                                                                                                                 |
| 1121 | TCGCGCGCGG TGTCATCTAT GTTACTAGAT CGATAAGCTT CTAGAGCGGC CGGTGGAGCT CCAATTCGCC                                                                              |
| 1191 | CTATAGTGAG TCGTATTACG CGCGCTCACT GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC                                                                              |
| 1261 | GTTACCCAAC TTAATCGCCT TGCAGCACAT CCCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA                                                                              |
| 1331 | CCGATCGCCC TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGGACGCG CCCTGTAGCG GCGCATTAAG                                                                              |
| 1401 | CGCGGCGGGT GTGGTGGTTA CGCGCAGCGT GACCGCTACA CTTGCCAGCG CCCTAGCGCC CGCTCCTTTC                                                                              |
| 1471 | GCTTTCTTCC CTTCCTTTCT CGCCACGTTC GCCGGCTTTC CCCGTCAAGC TCTAAATCGG GGGCTCCCTT                                                                              |

## Figure <u>3</u>C

|                                                                                                                                                                      |                                                                                                                                                                                                                               |                                                                                                                                                                                                                                                 |                                                                                                                                                                                                                                                                                               |                                                                                                                                                                                                                                |                                                                                                                                                                                                                              | ma acamaa ma                                                                                                                                                                                                              | amman aamna                                                                                                                                                                                                                                                          |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1541                                                                                                                                                                 | TAGGGTTCCG                                                                                                                                                                                                                    | ATTTAGTGCT                                                                                                                                                                                                                                      | TTACGGCACC                                                                                                                                                                                                                                                                                    | TCGACCCCAA                                                                                                                                                                                                                     | AAAAC'I"I'GAT                                                                                                                                                                                                                | TAGGGTGATG                                                                                                                                                                                                                | GTTCACGTAG                                                                                                                                                                                                                                                           |
| 1611                                                                                                                                                                 | TGGGCCATCG                                                                                                                                                                                                                    | CCCTGATAGA                                                                                                                                                                                                                                      | CGGTTTTTCG                                                                                                                                                                                                                                                                                    | CCCTTTGACG                                                                                                                                                                                                                     | TTGGAGTCCA                                                                                                                                                                                                                   | CGTTCTTTAA                                                                                                                                                                                                                | TAGTGGACTC                                                                                                                                                                                                                                                           |
| 1681                                                                                                                                                                 | TTGTTCCAAA                                                                                                                                                                                                                    | CTGGAACAAC                                                                                                                                                                                                                                      | ACTCAACCCT                                                                                                                                                                                                                                                                                    | ATCTCGGTCT                                                                                                                                                                                                                     | ATTCTTTTGA                                                                                                                                                                                                                   | TTTATAAGGG                                                                                                                                                                                                                | ATTTTGCCGA                                                                                                                                                                                                                                                           |
| 1751                                                                                                                                                                 | TTTCGGCCTA                                                                                                                                                                                                                    | TTGGTTAAAA                                                                                                                                                                                                                                      | AATGAGCTGA                                                                                                                                                                                                                                                                                    | TTTAACAAAA                                                                                                                                                                                                                     | ATTTAACGCG                                                                                                                                                                                                                   | AATTTTAACA                                                                                                                                                                                                                | AAATATTAAC                                                                                                                                                                                                                                                           |
| 1821                                                                                                                                                                 | GCTTACAATT                                                                                                                                                                                                                    | TAGGTGGCAC                                                                                                                                                                                                                                      | TTTTCGGGGA                                                                                                                                                                                                                                                                                    | AATGTGCGCG                                                                                                                                                                                                                     | GAACCCCTAT                                                                                                                                                                                                                   | TTGTTTATTT                                                                                                                                                                                                                | TTCTAAATAC                                                                                                                                                                                                                                                           |
| 1891                                                                                                                                                                 | ATTCAAATAT                                                                                                                                                                                                                    | GTATCCGCTC                                                                                                                                                                                                                                      | ATGAGACAAT                                                                                                                                                                                                                                                                                    | AACCCTGATA                                                                                                                                                                                                                     | AATGCTTCAA                                                                                                                                                                                                                   | TAATATTGAA                                                                                                                                                                                                                | AAAGGAAGAG                                                                                                                                                                                                                                                           |
| 1961                                                                                                                                                                 | TATGAGTATT                                                                                                                                                                                                                    | CAACATTTCC                                                                                                                                                                                                                                      | GTGTCGCCCT                                                                                                                                                                                                                                                                                    | TATTCCCTTT                                                                                                                                                                                                                     | TTTGCGGCAT                                                                                                                                                                                                                   | TTTGCCTTCC                                                                                                                                                                                                                | TGTTTTTGCT                                                                                                                                                                                                                                                           |
| 2031                                                                                                                                                                 | CACCCAGAAA                                                                                                                                                                                                                    | CGCTGGTGAA                                                                                                                                                                                                                                      | AGTAAAAGAT                                                                                                                                                                                                                                                                                    | GCTGAAGATC                                                                                                                                                                                                                     | AGTTGGGTGC                                                                                                                                                                                                                   | ACGAGTGGGT                                                                                                                                                                                                                | TACATCGAAC                                                                                                                                                                                                                                                           |
|                                                                                                                                                                      | TCCATCTCAA                                                                                                                                                                                                                    | CAGCGGTAAG                                                                                                                                                                                                                                      | ATCCTTGAGA                                                                                                                                                                                                                                                                                    | GTTTTCGCCC                                                                                                                                                                                                                     | CGAAGAACGT                                                                                                                                                                                                                   | TTTCCAATGA                                                                                                                                                                                                                | TGAGCACTTT                                                                                                                                                                                                                                                           |
| 2101                                                                                                                                                                 | TANACTTCTC                                                                                                                                                                                                                    | CTATGTGGCG                                                                                                                                                                                                                                      | CCCTATTATC                                                                                                                                                                                                                                                                                    | CCGTATTGAC                                                                                                                                                                                                                     | GCCGGGCAAG                                                                                                                                                                                                                   | AGCAACTCGG                                                                                                                                                                                                                | TCGCCGCATA                                                                                                                                                                                                                                                           |
| 2171                                                                                                                                                                 | CACHARGITCIC                                                                                                                                                                                                                  | AGAATGACTT                                                                                                                                                                                                                                      | CCTTCACTAC                                                                                                                                                                                                                                                                                    | TCACCACTCA                                                                                                                                                                                                                     | CAGAAAAGCA                                                                                                                                                                                                                   | TCTTACGGAT                                                                                                                                                                                                                | GGCATGACAG                                                                                                                                                                                                                                                           |
| 2241                                                                                                                                                                 | CACTATICIC                                                                                                                                                                                                                    | ATGCAGTGCT                                                                                                                                                                                                                                      | CCCATTACCA                                                                                                                                                                                                                                                                                    | TCACCACTCA                                                                                                                                                                                                                     | CACTCCCCCC                                                                                                                                                                                                                   | A A CTT A CTT C                                                                                                                                                                                                           | TGACAACGAT                                                                                                                                                                                                                                                           |
| 2311                                                                                                                                                                 | TAAGAGAATT                                                                                                                                                                                                                    | AAGGAGCTAA                                                                                                                                                                                                                                      | GCCATAACCA                                                                                                                                                                                                                                                                                    | CCACAACATC                                                                                                                                                                                                                     | CCCCATCATC                                                                                                                                                                                                                   | TAACTCCCCT                                                                                                                                                                                                                | TCATCCTTCC                                                                                                                                                                                                                                                           |
| 2381                                                                                                                                                                 | CGGAGGACCG                                                                                                                                                                                                                    | TGAATGAAGC                                                                                                                                                                                                                                      | CCGCIIIII                                                                                                                                                                                                                                                                                     | CACACCATC                                                                                                                                                                                                                      | ACACCACCAT                                                                                                                                                                                                                   | CCCTCTACCA                                                                                                                                                                                                                | ATGGCAACAA                                                                                                                                                                                                                                                           |
| 2451                                                                                                                                                                 | GAACCGGAGC                                                                                                                                                                                                                    | TGAATGAAGC                                                                                                                                                                                                                                      | CATACCAAAC                                                                                                                                                                                                                                                                                    | GACGAGCGIG                                                                                                                                                                                                                     | MEGGGGGGGA A                                                                                                                                                                                                                 | ADDATEDIOOD                                                                                                                                                                                                               | A CTICCA TCCA                                                                                                                                                                                                                                                        |
| 2521                                                                                                                                                                 | CGTTGCGCAA                                                                                                                                                                                                                    | ACTATTAACT                                                                                                                                                                                                                                      | GGCGAACTAC                                                                                                                                                                                                                                                                                    | TTACTCTAGC                                                                                                                                                                                                                     | TTCCCGGCAA                                                                                                                                                                                                                   | CAATTAATAG                                                                                                                                                                                                                | ACIGGAIGGA                                                                                                                                                                                                                                                           |
| 2591                                                                                                                                                                 | GGCGGATAAA                                                                                                                                                                                                                    | GTTGCAGGAC                                                                                                                                                                                                                                      | CACTTCTGCG                                                                                                                                                                                                                                                                                    | CTCGGCCCTT                                                                                                                                                                                                                     | CCGGCTGGCT                                                                                                                                                                                                                   | GGTTTATTGC                                                                                                                                                                                                                | TGATAAATCI                                                                                                                                                                                                                                                           |
| 2661                                                                                                                                                                 | GGAGCCGGTG                                                                                                                                                                                                                    | AGCGTGGGTC                                                                                                                                                                                                                                      | TCGCGGTATC                                                                                                                                                                                                                                                                                    | ATTGCAGCAC                                                                                                                                                                                                                     | TGGGGCCAGA                                                                                                                                                                                                                   | TGGTAAGCCC                                                                                                                                                                                                                | TCCCGTATCG                                                                                                                                                                                                                                                           |
| 2731                                                                                                                                                                 | TAGTTATCTA                                                                                                                                                                                                                    | CACGACGGGG                                                                                                                                                                                                                                      | AGTCAGGCAA                                                                                                                                                                                                                                                                                    | CTATGGATGA                                                                                                                                                                                                                     | ACGAAATAGA                                                                                                                                                                                                                   | CAGATCGCTG                                                                                                                                                                                                                | AGATAGGTGC                                                                                                                                                                                                                                                           |
| 2801                                                                                                                                                                 | CTCACTGATT                                                                                                                                                                                                                    | AAGCATTGGT                                                                                                                                                                                                                                      | AACTGTCAGA                                                                                                                                                                                                                                                                                    | CCAAGTTTAC                                                                                                                                                                                                                     | TCATATATAC                                                                                                                                                                                                                   | TTTAGATTGA                                                                                                                                                                                                                | TTTAAAACTT                                                                                                                                                                                                                                                           |
| 2871                                                                                                                                                                 | CATTTTTAAT                                                                                                                                                                                                                    | TTAAAAGGAT                                                                                                                                                                                                                                      | CTAGGTGAAG                                                                                                                                                                                                                                                                                    | ATCCTTTTTG                                                                                                                                                                                                                     | ATAATCTCAT                                                                                                                                                                                                                   | GACCAAAATC                                                                                                                                                                                                                | CCTTAACGTG                                                                                                                                                                                                                                                           |
| 2941                                                                                                                                                                 | AGTTTTCGTT                                                                                                                                                                                                                    | CCACTGAGCG                                                                                                                                                                                                                                      | TCAGACCCCG                                                                                                                                                                                                                                                                                    | TAGAAAAGAT                                                                                                                                                                                                                     | CAAAGGATCT                                                                                                                                                                                                                   | TCTTGAGATC                                                                                                                                                                                                                | CTTTTTTTCT                                                                                                                                                                                                                                                           |
| 3011                                                                                                                                                                 | GCGCGTAATC                                                                                                                                                                                                                    | TGCTGCTTGC                                                                                                                                                                                                                                      | AAACAAAAAA                                                                                                                                                                                                                                                                                    | ACCACCGCTA                                                                                                                                                                                                                     | CCAGCGGTGG                                                                                                                                                                                                                   | TTTGTTTGCC                                                                                                                                                                                                                | GGATCAAGAG                                                                                                                                                                                                                                                           |
| 3081                                                                                                                                                                 | CTACCAACTC                                                                                                                                                                                                                    | TTTTTCCGAA                                                                                                                                                                                                                                      | GGTAACTGGC                                                                                                                                                                                                                                                                                    | TTCAGCAGAG                                                                                                                                                                                                                     | CGCAGATACC                                                                                                                                                                                                                   | AAATACTGTC                                                                                                                                                                                                                | CTTCTAGTGT                                                                                                                                                                                                                                                           |
| 3151                                                                                                                                                                 | AGCCGTAGTT                                                                                                                                                                                                                    | AGGCCACCAC                                                                                                                                                                                                                                      | TTCAAGAACT                                                                                                                                                                                                                                                                                    | CTGTAGCACC                                                                                                                                                                                                                     | GCCTACATAC                                                                                                                                                                                                                   | CTCGCTCTGC                                                                                                                                                                                                                | TAATCCTGTT                                                                                                                                                                                                                                                           |
| 3221                                                                                                                                                                 | ACCAGTGGCT                                                                                                                                                                                                                    | GCTGCCAGTG                                                                                                                                                                                                                                      | GCGATAAGTC                                                                                                                                                                                                                                                                                    | GTGTCTTACC                                                                                                                                                                                                                     | GGGTTGGACT                                                                                                                                                                                                                   | CAAGACGATA                                                                                                                                                                                                                | GTTACCGGAT                                                                                                                                                                                                                                                           |
| 3291                                                                                                                                                                 | AAGGCGCAGC                                                                                                                                                                                                                    | GGTCGGGCTG                                                                                                                                                                                                                                      | AACGGGGGGT                                                                                                                                                                                                                                                                                    | TCGTGCACAC                                                                                                                                                                                                                     | AGCCCAGCTT                                                                                                                                                                                                                   | GGAGCGAACG                                                                                                                                                                                                                | ACCTACACCG                                                                                                                                                                                                                                                           |
| 3361                                                                                                                                                                 | AACTGAGATA                                                                                                                                                                                                                    | CCTACAGCGT                                                                                                                                                                                                                                      | GAGCTATGAG                                                                                                                                                                                                                                                                                    | AAAGCGCCAC                                                                                                                                                                                                                     | GCTTCCCGAA                                                                                                                                                                                                                   | GGGAGAAAGG                                                                                                                                                                                                                | CGGACAGGTA                                                                                                                                                                                                                                                           |
| 3431                                                                                                                                                                 | TCCGGTAAGC                                                                                                                                                                                                                    | GGCAGGGTCG                                                                                                                                                                                                                                      | GAACAGGAGA                                                                                                                                                                                                                                                                                    | GCGCACGAGG                                                                                                                                                                                                                     | GAGCTTCCAG                                                                                                                                                                                                                   | GGGGAAACGC                                                                                                                                                                                                                | CTGGTATCTT                                                                                                                                                                                                                                                           |
| 3501                                                                                                                                                                 | TATAGTCCTG                                                                                                                                                                                                                    | TCGGGTTTCG                                                                                                                                                                                                                                      | CCACCTCTGA                                                                                                                                                                                                                                                                                    | CTTGAGCGTC                                                                                                                                                                                                                     | GATTTTTGTG                                                                                                                                                                                                                   | ATGCTCGTCA                                                                                                                                                                                                                | GGGGGGCGGA                                                                                                                                                                                                                                                           |
|                                                                                                                                                                      | CCCTTTCCTC                                                                                                                                                                                                                    | 77700011100                                                                                                                                                                                                                                     | AACGCGGCCT                                                                                                                                                                                                                                                                                    | ጥጥጥ∆ CGGጥጥ                                                                                                                                                                                                                     | CCTGGCCTTT                                                                                                                                                                                                                   | TGCTGGCCTT                                                                                                                                                                                                                | TTGCTCACAT                                                                                                                                                                                                                                                           |
| 2 = 71                                                                                                                                                               |                                                                                                                                                                                                                               |                                                                                                                                                                                                                                                 |                                                                                                                                                                                                                                                                                               |                                                                                                                                                                                                                                |                                                                                                                                                                                                                              |                                                                                                                                                                                                                           |                                                                                                                                                                                                                                                                      |
| 3571                                                                                                                                                                 | CTATGGAA                                                                                                                                                                                                                      | CCCTTATCCC                                                                                                                                                                                                                                      | CTGATTCTGT                                                                                                                                                                                                                                                                                    | GGATAACCGT                                                                                                                                                                                                                     | ATTACCGCCT                                                                                                                                                                                                                   | TTGAGTGAGC                                                                                                                                                                                                                | TGATACCGCT                                                                                                                                                                                                                                                           |
| 3641                                                                                                                                                                 | GTTCTTTCCT                                                                                                                                                                                                                    | GCGTTATCCC                                                                                                                                                                                                                                      | CTGATTCTGT                                                                                                                                                                                                                                                                                    | GGATAACCGT                                                                                                                                                                                                                     | ATTACCGCCT                                                                                                                                                                                                                   | TTGAGTGAGC                                                                                                                                                                                                                | TGATACCGCT                                                                                                                                                                                                                                                           |
| 3641<br>3711                                                                                                                                                         | GTTCTTTCCT<br>CGCCGCAGCC                                                                                                                                                                                                      | GCGTTATCCC<br>GAACGACCGA                                                                                                                                                                                                                        | CTGATTCTGT<br>GCGCAGCGAG                                                                                                                                                                                                                                                                      | GGATAACCGT<br>TCAGTGAGCG                                                                                                                                                                                                       | ATTACCGCCT<br>AGGAAGCGGA                                                                                                                                                                                                     | TTGAGTGAGC<br>AGAGCGCCCA                                                                                                                                                                                                  | TGATACCGCT<br>ATACGCAAAC                                                                                                                                                                                                                                             |
| 3641<br>3711<br>3781                                                                                                                                                 | GTTCTTTCCT<br>CGCCGCAGCC<br>CGCCTCTCCC                                                                                                                                                                                        | GCGTTATCCC<br>GAACGACCGA<br>CGCGCGTTGG                                                                                                                                                                                                          | CTGATTCTGT<br>GCGCAGCGAG<br>CCGATTCATT                                                                                                                                                                                                                                                        | GGATAACCGT<br>TCAGTGAGCG<br>AATGCAGCTG                                                                                                                                                                                         | ATTACCGCCT<br>AGGAAGCGGA<br>GCACGACAGG                                                                                                                                                                                       | TTGAGTGAGC<br>AGAGCGCCCA<br>TTTCCCGACT                                                                                                                                                                                    | TGATACCGCT<br>ATACGCAAAC<br>GGAAAGCGGG                                                                                                                                                                                                                               |
| 3641<br>3711<br>3781<br>3851                                                                                                                                         | GTTCTTTCCT<br>CGCCGCAGCC<br>CGCCTCTCCC<br>CAGTGAGCGC                                                                                                                                                                          | GCGTTATCCC<br>GAACGACCGA<br>CGCGCGTTGG<br>AACGCAATTA                                                                                                                                                                                            | CTGATTCTGT<br>GCGCAGCGAG<br>CCGATTCATT<br>ATGTGAGTTA                                                                                                                                                                                                                                          | GGATAACCGT<br>TCAGTGAGCG<br>AATGCAGCTG<br>GCTCACTCAT                                                                                                                                                                           | ATTACCGCCT<br>AGGAAGCGGA<br>GCACGACAGG<br>TAGGCACCCC                                                                                                                                                                         | TTGAGTGAGC<br>AGAGCGCCCA<br>TTTCCCGACT<br>AGGCTTTACA                                                                                                                                                                      | TGATACCGCT<br>ATACGCAAAC<br>GGAAAGCGGG<br>CTTTATGCTT                                                                                                                                                                                                                 |
| 3641<br>3711<br>3781                                                                                                                                                 | GTTCTTTCCT<br>CGCCGCAGCC<br>CGCCTCTCCC<br>CAGTGAGCGC                                                                                                                                                                          | GCGTTATCCC<br>GAACGACCGA<br>CGCGCGTTGG                                                                                                                                                                                                          | CTGATTCTGT<br>GCGCAGCGAG<br>CCGATTCATT<br>ATGTGAGTTA                                                                                                                                                                                                                                          | GGATAACCGT<br>TCAGTGAGCG<br>AATGCAGCTG<br>GCTCACTCAT                                                                                                                                                                           | ATTACCGCCT<br>AGGAAGCGGA<br>GCACGACAGG<br>TAGGCACCCC<br>TTCACACAGG                                                                                                                                                           | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT                                                                                                                                                                    | TGATACCGCT<br>ATACGCAAAC<br>GGAAAGCGGG<br>CTTTATGCTT<br>GACCATGATT                                                                                                                                                                                                   |
| 3641<br>3711<br>3781<br>3851                                                                                                                                         | GTTCTTTCCT<br>CGCCGCAGCC<br>CGCCTCTCCC<br>CAGTGAGCGC                                                                                                                                                                          | GCGTTATCCC<br>GAACGACCGA<br>CGCGCGTTGG<br>AACGCAATTA                                                                                                                                                                                            | CTGATTCTGT<br>GCGCAGCGAG<br>CCGATTCATT<br>ATGTGAGTTA                                                                                                                                                                                                                                          | GGATAACCGT<br>TCAGTGAGCG<br>AATGCAGCTG<br>GCTCACTCAT                                                                                                                                                                           | ATTACCGCCT<br>AGGAAGCGGA<br>GCACGACAGG<br>TAGGCACCCC<br>TTCACACAGG<br>KpnI                                                                                                                                                   | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT                                                                                                                                                                    | TGATACCGCT<br>ATACGCAAAC<br>GGAAAGCGGG<br>CTTTATGCTT<br>GACCATGATT<br>XhoI                                                                                                                                                                                           |
| 3641<br>3711<br>3781<br>3851<br>3921                                                                                                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA                                                                                                                                                                        | GCGTTATCCC<br>GAACGACCGA<br>CGCGCGTTGG<br>AACGCAATTA<br>TGTTGTGTGG                                                                                                                                                                              | CTGATTCTGT<br>GCGCAGCGAG<br>CCGATTCATT<br>ATGTGAGTTA<br>AATTGTGAGC                                                                                                                                                                                                                            | GGATAACCGT<br>TCAGTGAGCG<br>AATGCAGCTG<br>GCTCACTCAT<br>GGATAACAAT                                                                                                                                                             | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI                                                                                                                                                                  | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT                                                                                                                                                                    | TGATACCGCT<br>ATACGCAAAC<br>GGAAAGCGGG<br>CTTTATGCTT<br>GACCATGATT<br>XhoI                                                                                                                                                                                           |
| 3641<br>3711<br>3781<br>3851<br>3921                                                                                                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA                                                                                                                                                                        | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGGG                                                                                                                                                                                         | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC CCTCACTAAA                                                                                                                                                                                                                             | GGATAACCGT<br>TCAGTGAGCG<br>AATGCAGCTG<br>GCTCACTCAT<br>GGATAACAAT                                                                                                                                                             | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC                                                                                                                                                       | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  ~ GGGCCCCCCC                                                                                                                                                      | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT                                                                                                                                                                                               |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061                                                                                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA ACGCCAAGCG                                                                                                                                                             | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG CGCAATTAAC                                                                                                                                                                             | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC CCTCACTAAA TCGGGATAGT                                                                                                                                                                                                                  | GGATAACCGT<br>TCAGTGAGCG<br>AATGCAGCTG<br>GCTCACTCAT<br>GGATAACAAT<br>GGGAACAAAA<br>CCAAAATAAA                                                                                                                                 | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA                                                                                                                                            | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  CGGGCCCCCCC GATTACCTGG                                                                                                                                            | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA                                                                                                                                                                                    |
| 3641<br>3711<br>3781<br>3851<br>3921                                                                                                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT                                                                                                                                      | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG                                                                                                                                                       | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC CCTCACTAAA TCGGGATAGT TATAAGTAAA                                                                                                                                                                                                       | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAA                                                                                                                                        | ATTACCGCCT AGGAAGCGGA GCACGACACGC TAGGCACCCC TTCACACAGG KpnI CCTGGGTACC ACAAAGGTAA TAAAAGGTGG                                                                                                                                | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCCC GATTACCTGG CCCAAAGTGA                                                                                                                                  | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA AATTTACTCT                                                                                                                                                                         |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061                                                                                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT                                                                                                                                      | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG                                                                                                                                                      | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGCTTA AATTGTGAGC CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT                                                                                                                                                                                           | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAA TGTCGGTACT                                                                                                                             | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG                                                                                                                                           | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT                                                                                                                       | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT                                                                                                                                                              |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131                                                                                                         | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT                                                                                                                           | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG                                                                                                                                | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGCTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA                                                                                                                                                                               | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAA TGTCGGTACT TCTGTATTTG                                                                                                                  | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT                                                                                                                     | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT                                                                                                             | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA                                                                                                                                                   |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201                                                                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT                                                                                                                           | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG                                                                                                                                | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT                                                                                                                                                                     | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAA TGTCGGTACT TCTGTATTTG                                                                                                                  | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT                                                                                                                     | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT                                                                                                             | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA                                                                                                                                                   |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271                                                                                         | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT                                                                                                                           | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG                                                                                                                                | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT                                                                                                                                                                     | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAA TGTCGGTACT TCTGTATTTG                                                                                                                  | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT                                                                                                                     | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT                                                                                                             | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA                                                                                                                                                   |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271                                                                                         | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG                                                                                                     | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI                                                                                                               | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGCTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT                                                                                                                                                                    | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TGTCGGTACT TCTGTATTTG                                                                                                                 | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT                                                                                                          | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT                                                                                                 | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA                                                                                                                                        |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271                                                                                         | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG                                                                                                     | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI ~~~~~                                                                                                         | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGCTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  ~~ CCACAATGAA                                                                                                                                                     | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCCC                                                                                                                | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI CCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT                                                                                                | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCC                                                                                     | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA                                                                                                                                        |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341                                                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG                                                                                                     | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI CAGGCGAATT                                                                                                    | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGCTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  ~~ CCACAATGAA TAAAAGATAA                                                                                                                                          | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCCC CAATAATAAG ACTTAGACTCC                                                                                         | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI CCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATTAAAATAG                                                                                               | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC                                                                           | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC                                                                                                      |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341                                                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT GGGTATTTTT CTAAAGCCCA                                                                   | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI CAGGCGAATT TCTAGTAAAA AAGTGCTATG                                                                              | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGCTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAAGATAA CACGATCCAT                                                                                                                                  | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCC CAATAATAAG ACTTAGACTC AGCAAGCCCA                                                                                | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI CCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATTAAAATAG AAAACATTTA GCCCAACCCA                                                                         | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                                | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCCA                                                                                           |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341                                                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT GGGTATTTTT CTAAAGCCCA                                                                   | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI CAGGCGAATT TCTAGTAAAA AAGTGCTATG CTGGCAATAG                                                                   | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGCTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAAGATAA CACGATCCAT GTCTCCACCC                                                                                                                       | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCC CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT                                                                     | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI ————— GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT  ATTAAAATAG AAAACATTTA GCCCAACCCA CACCAGGT                                                         | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                                | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTTGCAGCGAT CCCTAAAGTC ACCCACCCCA ACCGCACGTC                                                                                         |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621                                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT GGGTATTTTT CTAAAGCCCA GTGCAGCCAA                                                        | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI CAGGCGAATT TCTAGTAAAA AAGTGCTATG CTGGCAAATA                                                                   | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGCTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAAGATAA CACGATCCAT GTCTCCACCC                                                                                                                       | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCC  CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA                                                         | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATTAAAATAG AAAACATTTA GCCCAACCCA CACCGTGAGT GAAAACAGG                                                    | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                               | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTTGCAGCGAT CCCTAAAGTC ACCCACCCCA ACCGCACGTC GGGTCGTGGG                                                                              |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551                                                         | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT CTAAAGCCCA GTGCAGCCAA GGCCGGAAAA                                                        | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI TCTAGTAAAA AAGTGCTATG CTGGCAAATA AAGTGCTATG CTGGCAAATA AAAAAAAAAA                                             | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGCTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAAGATAA CACGATCCAT GTCTCCACCC AGAAAGAAAA                                                                                                            | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA ATATCGGTAAA TGTCGGTACT TCTGTATTTG TAAAAAAACCCC CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGAGGCCC                                            | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATTAAAATAG AAAACATTTA GCCCAACCCA CACCGTGAGT GAAAACAGC                                                    | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                               | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTTGCAGCGAT CCCTAAAGTC ACCCACCCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC                                                                   |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761                                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT CTAAAGCCCA GTGCAGCCAA GGCCGGAAAA                                                        | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA CAGGCGAATT CAGGCGAATT CTAGTAAAA AAGTGCTATG CTGGCAAATA AAAAAAAAAA                                                    | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAAGATAA CACGATCCAT GTCTCCACCC AGAAAGAAAA TCGCGAGCAG                                                                                                  | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAAACCCC CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGAGGCC TCTCCTCCCA                                  | ATTACCGCCT AGGAAGCGGA GCACGACACGC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATTAAAATAG AAAACATTTA GCCCAACCCA CACCGTGAGT GAAAACAGC                                                    | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                               | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC CCACCACCCC CCCCACCACCCC                                            |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831                         | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT CTAAAGCCCA GTGCAGCCAA GCCCGGAAAA CCCCATCGCC CACCTCCTCC                                  | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA CAGGCGAATT CTAGTAAAA AAGTGCTATG CTGGCAAATA AAAAAAAAAA                                                               | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAAGATAA CACGATCCAT GTCTCCACCC AGAAAGAAAA TCGCGAGCAG TACCCCCCCC                                                                                       | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCC  CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGAGGCC TCTCCTCCCA AGCTCCTCCCA                       | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATTAAAATAG AAAACATTTA GCCCAACCCA CACCGTGAGT GAAAACAGGC CGGCCCTCCCCT                            | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                               | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC CCACCACCAC CCGCTAACCAC                                             |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT CTAAAGCCCA GTGCAGCCAA GCCCGGAAAA CCCCATCGCC CACCTCCTCC                                  | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA CAGGCGAATT CTAGTAAAA AAGTGCTATG CTGGCAAATA AAAAAAAAAA                                                               | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAAGATAA CACGATCCAT GTCTCCACCC AGAAAGAAAA TCGCGAGCAG TACCCCCCCC                                                                                       | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCC  CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGAGGCC TCTCCTCCCA AGCTCCTCCCA                       | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATTAAAATAG AAAACATTTA GCCCAACCCA CACCGTGAGT GAAAACAGGC CGGCCCTCCCCT                            | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCCC GATTACCTGG CCCAAAGTGA ATTTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                               | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC CCACCACCCC CCACCACCCC CCGCTAACCCC CCACCACCCC CCACCACCCC CCACCACCAC |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971         | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT CTAAAGCCCA GTGCAGCCAA GCCCGGAAAA CCCCATCGCC CACCTCCTCC                                  | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA CAGGCGAATT CTAGTAAAA AAGTGCTATG CTGGCAAATA AAAAAAAAA AACGGAGGGGAGA ACTATATACA CCCCCTCGCTG                           | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA CCACAATGAA TAAAAGATAA CACGATCCAT GTCTCCACCC AGAAAGAAAA TCGCGAGCAG TACCCCCCCC CCGGACGACG                                                                                        | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCC  CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGAGGCC TCTCCTCCCA AGCTCCTCCCA TTTTTTTCGT            | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATTAAAATAG AAAACATTTA GCCCAACCCA CACCGTGAGT GAAAACAGC CCCCCCCCCC                               | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                                 | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC CCACCACCAC CCGCTAACCAC TTGGTAGTTT                                   |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901                 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT CTAAAGCCCA GTGCAGCCAA GCCCGGAAAA CCCCATCGCC CACCTCCTCC                                  | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI CAGGCGAATT CTAGTAAAA AAGTGCTATG CTGGCAAATA AAAAAAAAA CGCGAGGGGGGG ACTATATACA CCCCCCCGCTG TCCTCTTCT GAGCGGCTTC | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAGATAA CACGATCCAT GTCTCCACCC AGAAAGAAAA TCGCGAGCAG TACCCCCCCC CCGGACGACG TTCTCCGTTT GTCGCCCAGA                                                       | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCC  CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGAGGCC TCTCCTCCCA AGCTCCTCCCA TTTTTTTCGT            | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATAAAATAG AAAACATTTA GCCCAACCCA CACCGTGAGT GAAAAACAGC CCGCCCCCCC TCCCCCCCCCC                   | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                                 | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC CCACCACCCC CCACCACCCC CCGCTAACCCC CCACCACCCC CCACCACCCC CCACCACCAC |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971         | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT CTAAAGCCCA GTGCAGCCAA GCCCGGAAAA CCCCATCGCC CACCTCCTCC                                  | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA CCGGCGAATT CTAGTAAAA AAGTGCTATG CTGGCAAATA AAAAAAAAA AGCGAGGAGGA CCCCCCGCTG TCCTCTTTCT GAGCGGCTTC                   | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAGATAA CACGATCCAT GTCTCCACCC AGAAAGAAAA TCGCGAGCAG TACCCCCCCC CCGGACGACG TTCTCCGTTT GTCGCCCAGA                                                       | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA CCAAAATAAA ATATCGGTAAT TCTGTATTTG TAAAAAACCC  CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGAGGCC TCTCCTCCCA AGCTCCTCCCA TTTTTTTCGT            | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT GCCCAACCCA CACCGTGAGT GAAAACAGCC CCCCCCCCCC                                                    | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                                 | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC CCACCACCAC CCGCTAACCAC TTGGTAGTTT                                   |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971<br>5041 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  GGCTGAGCCAA CCCCATCGCC CACCTCCTCC GGGTGGGGCGAA                                                     | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA CAGGCGAATT CTAGTAAAA AAGTGCTATG AAAAAAAAAA                                                                          | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA CACGATCCAT GTCTCCACCO AGAAAGAAAA TCGCGAGCAG TACCCCCCCC CCGGACGACG TTCTCCGTTT GTCGCCCAGA HI                                                                                     | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT GGGAACAAAA ATATCGGTAAA TGTCGGTACT TCTGTATTTG TAAAAAACCC  CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGAGGCC TCTCCTCCCA AGCTCCTCCCA TCGGTGCGCGC           | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATGCTAAT ATTAAAATAG AAAACATTTA GCCCAACCCA CACCGTGAGT GAAAAACAGC CCCCCCCCCC                              | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAAC ACCCAACCCA                                                                 | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC CCACCACCAC CCGGTAACCAC TTGGTAGTTT CTTGGCGTCTC                       |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971<br>5041 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT CTAAAGCCCA GGCCGGAAAA CCCCATCGCC CACCTCCTCC GGGTGGGCGA                                  | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI CAGGCGAATT CAGGCAATTA CTGGCAATAA AAAAAAAAA ACTGCTATG AAAAAAAAAA                                               | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGTAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA CACGATCATA TAAAAGATAA CACGATCCAC AGAAAGAAAA TCGCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG                                                                                                     | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT  GGGAACAAAA ATATCGGTAA TGTCGGTACT TCTGTATTTG TAAAAAACCC  CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGGCC TCTCCTCCCA AGCTCCTCCCA TCTGTTTTTCGT TCGGTGCGCG | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATACTAAT AAAACATTA GCCCAACCCA CACCGTGAGT GAAAACACCC CGCCCTCCCCCCC CTCCGGTCTCG GGAGGGGCGGG E CTCCGGATGTA | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAC ACCAACCCA TGTCCGCACC AGGTGGGTCC CCTACCACCA CCGCCGCCGCGCGCGCGCGCGCGCGCGCGCGC | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT Xho I  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC CCACCACCAC CCGGTAACCAC TTGGTAGTTT CTGGCGTCTC                      |
| 3641<br>3711<br>3781<br>3851<br>3921<br>3991<br>4061<br>4131<br>4201<br>4271<br>4341<br>4411<br>4481<br>4551<br>4621<br>4691<br>4761<br>4831<br>4901<br>4971<br>5041 | GTTCTTTCCT CGCCGCAGCC CGCCTCTCCC CAGTGAGCGC CCGGCTCGTA  ACGCCAAGCG TCATATGCTT AAACATCAGT TTTCTACTAT TTAAGTTTAT ATACAGAGGG  AATATATATT CTAAAGCCCA GGCCGGAAAA CCCCATCGCC CACCTCCTCC GGGTGGGCGAA CCGGCCCTC GGGTGGGCGAA CCGGCCCTC | GCGTTATCCC GAACGACCGA CGCGCGTTGG AACGCAATTA TGTTGTGTGTGG  CGCAATTAAC GAGAAGAGAG TAAAAGGTGG TATAAAAATT TCGCGATTTG ATTTGTATAA ECORI CAGGCGAATT CAGGCAATTA CTGGCAATAA AAAAAAAAA ACTGCTATG AAAAAAAAAA                                               | CTGATTCTGT GCGCAGCGAG CCGATTCATT ATGTGAGTTA AATTGTGAGC  CCTCACTAAA TCGGGATAGT TATAAGTAAA GAGGATGTTT GAAATGCATA GAAATATCTT  CCACAATGAA TAAAAGATAA CACGATCCAT GTCTCCACCC AGAAAGAAAA TCGCGAGCAG TTCTCCGTTT GTCGCCCAGA HI CCCCCCGGGCCAGA HI CCCCCCGGGCCAGA CCCCCCGGGCCAGA CCCCCCCGGCCCCGGCCCCCCCC | GGATAACCGT TCAGTGAGCG AATGCAGCTG GCTCACTCAT GGATAACAAT  GGGAACAAAA ATATCGGTAA TGTCGGTACT TCTGTATTTG TAAAAAACCC  CAATAATAAG ACTTAGACTC AGCAAGCCCA CCGGCACTAT AAAAGAAAAA CGACGGCC TCTCCTCCCA AGCTCCTCCCA TCTGTTTTTCGT TCGGTGCGCG | ATTACCGCCT AGGAAGCGGA GCACGACAGG TAGGCACCCC TTCACACAGG KpnI GCTGGGTACC ACAAAGGTAA TAAAAGGTGG TTGATACGTC AGTCGGTTTT ATATACTAAT AAAACATTA GCCCAACCCA CACCGTGAGT GAAAACACCC CGCCCTCCCCCCC CTCCGGTCTCG GGAGGGGCGGG E CTCCGGATGTA | TTGAGTGAGC AGAGCGCCCA TTTCCCGACT AGGCTTTACA AAACAGCTAT  GGGCCCCCC GATTACCTGG CCCAAAGTGA ATTTTGTAT TAAGTTCGTT TTGACATAAT  CTTGCCCCCG CAAAAACAC ACCAACCCA TGTCCGCACC AGGTGGGTCC CCTACCACCA CCGCCGCCGCGCGCGCGCGCGCGCGCGCGCGC | TGATACCGCT ATACGCAAAC GGAAAGCGGG CTTTATGCTT GACCATGATT XhoI  TCGAGGTCAT TCAAAAGTGA AATTTACTCT GAATTGGTTT GCTTTTGTAA TTTTGAGAAA  TTGCAGCGAT CCCTAAAGTC ACCCACCCA ACCGCACGTC GGGTCGTGGG AAGAAACGCC CCACCACCAC CCGGTAACCAC TTGGTAGTTT CTTGGCGTCTC                       |

### Figure 38 A



#### Figure 38 B

#### BamHI

· I L R D D S S K E I I T V F R G T G S D T N L GATCCTCCGC GACGACAGCA GCAAAGAAAT AATCACCGTC TTCCGTGGCA CTGGTAGTGA TACGAATCTA Q L D T N Y T L T P F D T L P Q C N G C E V H G CAACTCGATA CTAACTACAC CCTCACGCCT TTCGACACCC TACCACAATG CAACGGTTGT GAAGTACACG . G Y Y I G W V S V Q D Q V E S L V K Q Q V S Q · 141 GTGGATATTA TATTGGATGG GTCTCCGTCC AGGACCAAGT CGAGTCGCTT GTCAAACAGC AGGTTAGCCA . Y P D Y A L T V T G H X L G A S L A A L T A A GTATCCGGAC TACGCGCTGA CCGTGACCGG CCACKCCCTC GGCGCCTCCC TGGCGGCACT CACTGCCGCC Q L S A T Y D N I R L Y T F G E P R S G N Q A F CAGCTGTCTG CGACATACGA CAACATCCGC CTGTACACCT TCGGCGAACC GCGCAGCGGC AATCAGGCCT 281 XhoI

- · ASY MND AFQASSP DTT QYFR VTH. 351 TCGCGTCGTA CATGAACGAT GCCTTCCAAG CCTCGAGCCC AGATACGACG CAGTATTTCC GGGTCACTCA NCOI
- · A N D G I P N L P P V E Q G Y A H G G V E Y W TGCCAACGAC GGCATCCCAA ACCTGCCCCC GGTGGAGCAG GGGTACGCCC ATGGCGGTGT AGAGTACTGG  $\begin{smallmatrix} S & V & D & P & Y & S & A & Q & N & T & F & V & C & T & G & D & E & V & Q & C & C & E & A & Q \\ \end{smallmatrix}$ · G G Q G V N N A H T T Y F G M T S G A C T W \* · AGGGCGGACA GGGTGTGAAT AATGCGCACA CGACTTATTT TGGGATGACG AGCGGAGCCT GTACATGGTG ATCAGTCATT TCAGCCTCCC CGAGTGTACC AGGAAAGATG GATGTCCTGG AGAGGGGGCC GCGTAACCAC 631 TGAAGGATGA GCTGTAAAGA AGCAGATCGT TCAAACATTT GGCAATAAAG TTTCTTAAGA TTGAATCCTG 701 TTGCCGGTCT TGCGATGATT ATCATATAAT TTCTGTTGAA TTACGTTAAG CATGTAATAA TTAACATGTA 771 ATGCATGACG TTATTTATGA GATGGGTTTT TATGATTAGA GTCCCGCAAT TATACATTTA ATACGCGATA 841 GAAAACAAAA TATAGCGCGC AAACTAGGAT AAATTATCGC GCGCGGTGTC ATCTATGTTA CTAGATCGAT

#### 911 XbaI

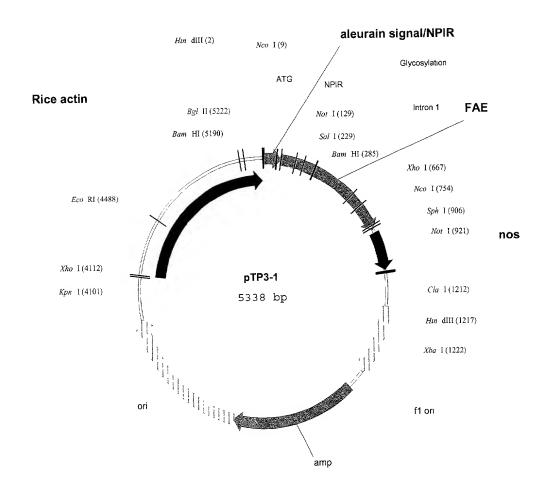
#### HindIII

|      |            |            | ~          | ~~~~       |            |            |            |
|------|------------|------------|------------|------------|------------|------------|------------|
| 981  | AAGCTTCTAG | AGCGGCCGGT | GGAGCTCCAA | TTCGCCCTAT | AGTGAGTCGT | ATTACGCGCG | CTCACTGGCC |
| 1051 | GTCGTTTTAC | AACGTCGTGA | CTGGGAAAAC | CCTGGCGTTA | CCCAACTTAA | TCGCCTTGCA | GCACATCCCC |
| 1121 | CTTTCGCCAG | CTGGCGTAAT | AGCGAAGAGG | CCCGCACCGA | TCGCCCTTCC | CAACAGTTGC | GCAGCCTGAA |
| 1191 | TGGCGAATGG | GACGCGCCCT | GTAGCGGCGC | ATTAAGCGCG | GCGGGTGTGG | TGGTTACGCG | CAGCGTGACC |
| 1261 | GCTACACTTG | CCAGCGCCCT | AGCGCCCGCT | CCTTTCGCTT | TCTTCCCTTC | CTTTCTCGCC | ACGTTCGCCG |
| 1331 | GCTTTCCCCG | TCAAGCTCTA | AATCGGGGGC | TCCCTTTAGG | GTTCCGATTT | AGTGCTTTAC | GGCACCTCGA |
| 1401 | CCCCAAAAAA | CTTGATTAGG | GTGATGGTTC | ACGTAGTGGG | CCATCGCCCT | GATAGACGGT | TTTTCGCCCT |
| 1471 | TTGACGTTGG | AGTCCACGTT | CTTTAATAGT | GGACTCTTGT | TCCAAACTGG | AACAACACTC | AACCCTATCT |
| 1541 | CGGTCTATTC | TTTTGATTTA | TAAGGGATTT | TGCCGATTTC | GGCCTATTGG | TTAAAAAATG | AGCTGATTTA |
| 1611 | ACAAAAATTT | AACGCGAATT | TTAACAAAAT | ATTAACGCTT | ACAATTTAGG | TGGCACTTTT | CGGGGAAATG |
| 1681 | TGCGCGGAAC | CCCTATTTGT | TTATTTTTCT | AAATACATTC | AAATATGTAT | CCGCTCATGA | GACAATAACC |
| 1751 | CTGATAAATG | CTTCAATAAT | ATTGAAAAAG | GAAGAGTATG | AGTATTCAAC | ATTTCCGTGT | CGCCCTTATT |
| 1821 | CCCTTTTTTG | CGGCATTTTG | CCTTCCTGTT | TTTGCTCACC | CAGAAACGCT | GGTGAAAGTA | AAAGATGCTG |
| 1891 | AAGATCAGTT | GGGTGCACGA | GTGGGTTACA | TCGAACTGGA | TCTCAACAGC | GGTAAGATCC | TTGAGAGTTT |
| 1961 | TCGCCCCGAA | GAACGTTTTC | CAATGATGAG | CACTTTTAAA | GTTCTGCTAT | GTGGCGCGGT | ATTATCCCGT |
| 2031 | ATTGACGCCG | GGCAAGAGCA | ACTCGGTCGC | CGCATACACT | ATTCTCAGAA | TGACTTGGTT | GAGTACTCAC |
| 2101 | CAGTCACAGA | AAAGCATCTT | ACGGATGGCA | TGACAGTAAG | AGAATTATGC | AGTGCTGCCA | TAACCATGAG |
| 2171 | TGATAACACT | GCGGCCAACT | TACTTCTGAC | AACGATCGGA | GGACCGAAGG | AGCTAACCGC | TTTTTTGCAC |
| 2241 | AACATGGGGG | ATCATGTAAC | TCGCCTTGAT | CGTTGGGAAC | CGGAGCTGAA | TGAAGCCATA |            |
| 2311 | AGCGTGACAC | CACGATGCCT | GTAGCAATGG | CAACAACGTT | GCGCAAACTA | TTAACTGGCG | AACTACTTAC |
| 2381 | TCTAGCTTCC | CGGCAACAAT | TAATAGACTG | GATGGAGGCG | GATAAAGTTG | CAGGACCACT | TCTGCGCTCG |
| 2451 | GCCCTTCCGG | CTGGCTGGTT | TATTGCTGAT | AAATCTGGAG | CCGGTGAGCG | TGGGTCTCGC | GGTATCATTG |
| 2521 | CAGCACTGGG | GCCAGATGGT | AAGCCCTCCC | GTATCGTAGT | TATCTACACG | ACGGGGAGTC | AGGCAACTAT |
| 2591 | GGATGAACGA | AATAGACAGA | TCGCTGAGAT | AGGTGCCTCA | CTGATTAAGC | ATTGGTAACT | GTCAGACCAA |
| 2661 | GTTTACTCAT | ATATACTTTA | GATTGATTTA | AAACTTCATT | TTTAATTTAA | AAGGATCTAG | GTGAAGATCC |
|      |            |            |            |            |            |            |            |

## Figure <u>38</u> C

| 2731 | TTTTTGATAA TCTCATGACC AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA                                                                                   |
|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 2801 | AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAAACCA                                                                                   |
| 2871 | CCGCTACCAG CGGTGGTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTTCA                                                                                   |
| 2941 | GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC CACCACTTCA AGAACTCTGT                                                                                   |
| 3011 | AGCACCGCCT ACATACCTCG CTCTGCTAAT CCTGTTACCA GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT                                                                                   |
| 3081 | CTTACCGGGT TGGACTCAAG ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT                                                                                   |
| 3151 | GCACACAGCC CAGCTTGGAG CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC TATGAGAAAG                                                                                   |
| 3221 | CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC                                                                                   |
|      | ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG GTTTCGCCAC CTCTGACTTG                                                                                   |
| 3291 | ACGAGGGAGC TTCCAGGGG MAACGCCTGG MTGCTTTTTTTTTTTTTTTTTTTTTTTTTTTT                                                                                               |
| 3361 | ACGCTCCTG GCCTTTTGCT GGCCTTTTGC TCACATGTTC TTTCCTGCGT TATCCCCTGA TTCTGTGGAT                                                                                    |
| 3431 | AACCGTATTA CCGCCTTTGA GTGAGCTGAT ACCGCTCGCC GCAGCCGAAC GACCGAGCGC AGCGAGTCAG                                                                                   |
| 3501 | TGAGCGAGGA AGCGGAAGAG CGCCCAATAC GCAAACCGCC TCTCCCCGCG CGTTGGCCGA TTCATTAATG                                                                                   |
| 3571 | TGAGCGAGGA AGCGGAAGAG CGCCCAATAC GCAAACCGCC TCTCCCCGGG CGTTGGCCGA TTCATTATTG CAGCTGGCAC GACAGGTTTC CCGACTGGAA AGCGGGCAGT GAGCGCAACG CAATTAATGT GAGTTAGCTC      |
| 3641 | CAGCTGGCAC GACAGGTTTC CCGACTGGAA AGCGGGCAGC GAGCGAACG CAATTAATGT GAGTGACTCAT                                                                                   |
| 3711 | ACTCATTAGG CACCCCAGGC TTTACACTTT ATGCTTCCGG CTCGTATGTT GTGTGGAATT GTGAGCGGAT                                                                                   |
| 3781 | AACAATTTCA CACAGGAAAC AGCTATGACC ATGATTACGC CAAGCGCGCA ATTAACCCTC ACTAAAGGGA                                                                                   |
|      | KpnI XhoI                                                                                                                                                      |
|      | ~~~~~                                                                                                                                                          |
| 3851 | ACAAAAGCTG GGTACCGGGC CCCCCTCGA GGTCATTCAT ATGCTTGAGA AGAGAGTCGG GATAGTCCAA                                                                                    |
| 3921 | AATAAAACAA AGGTAAGATT ACCTGGTCAA AAGTGAAAAC ATCAGTTAAA AGGTGGTATA AGTAAAATAT                                                                                   |
| 3991 | CGGTAATAAA AGGTGGCCCA AAGTGAAATT TACTCTTTTC TACTATTATA AAAATTGAGG ATGTTTTGTC                                                                                   |
| 4061 | GGTACTTTGA TACGTCATTT TTGTATGAAT TGGTTTTTAA GTTTATTCGC GATTTGGAAA TGCATATCTG                                                                                   |
| 4131 | TATTTGAGTC GGTTTTTAAG TTCGTTGCTT TTGTAAATAC AGAGGGATTT GTATAAGAAA TATCTTTAAA                                                                                   |
| 4131 | EcoRI                                                                                                                                                          |
|      | ~~~~~                                                                                                                                                          |
| 4201 | AAACCCATAT GCTAATTTGA CATAATTTTT GAGAAAAATA TATATTCAGG CGAATTCCAC AATGAACAAT                                                                                   |
| 4201 | AATAAGATTA AAATAGCTTG CCCCCGTTGC AGCGATGGGT ATTTTTCTA GTAAAATAAA AGATAAACTT                                                                                    |
|      | AGACTCAAAA CATTTACAAA AACAACCCCT AAAGTCCTAA AGCCCAAAGT GCTATGCACG ATCCATAGCA                                                                                   |
| 4341 | AGCCCAGCCC AACCCAACCC ACCCCAGTGC AGCCAACTGG CAAATAGTCT CCACCCCCGG                                                                                              |
| 4411 | CACTATCACC GTGAGTTGTC CGCACCACCG CACGTCTCGC AGCCAAAAAA AAAAAAAGAA AGAAAAAAAA                                                                                   |
| 4481 | GAAAAAGAAA AACAGCAGGT GGGTCCGGGT CGTGGGGGCC GGAAAAGCGA GGAGGATCGC GAGCAGCGAC                                                                                   |
| 4551 | GAAAAAGAAA AACAGCAGGT GGGTCCGGGT CGTGGGGGGCC GGAAAAGCGA GGAGGATCGC GACCACCTCCC<br>GAGGCCCGGC CCTCCCTCCG CTTCCAAAGA AACGCCCCCC ATCGCCACTA TATACATACC CCCCCCTCTC |
| 4621 | GAGGCCCGGC CCTCCCTCCG CTTCCAAAGA AACGCCCCCC ATCGCCACTA TATACAATCA ACGCCCCCC                                                                                    |
| 4691 | CTCCCATCCC CCCAACCCTA CCACCACCAC CACCACCAC TCCTCCCCCC TCGCTGCCGG ACGACGAGCT                                                                                    |
| 4761 | CCTCCCCCT CCCCTCCGC CGCCGCCGGT AACCACCCCG CCCCTCTCCT CTTTCTTTCT CCGTTTTTTT                                                                                     |
| 4831 | TTTCGTCTCG GTCTCGATCT TTGGCCTTGG TAGTTTGGGT GGGCGAGAGC GGCTTCGTCG CCCAGATCGG                                                                                   |
|      | BamHI                                                                                                                                                          |
|      | ~~~~~                                                                                                                                                          |
| 4901 | TGCGCGGGAG GGGCGGGATC TCGCGGCTGG CGTCTCCGGG CGTGAGTCGG CCCGGATCCT CGCGGGGAAT                                                                                   |
|      | BglII                                                                                                                                                          |
|      | ~~~~                                                                                                                                                           |
| 4971 | GGGGCTCTCG GATGTAGATC TTCTTTCTTT CTTCTTTTTG TGGTAGAATT TGAATCCCTC AGCATTGTTC                                                                                   |
|      | HindIII                                                                                                                                                        |
|      | ~                                                                                                                                                              |
| 5041 | ATCGGTAGTT TTTCTTTCA TGATTTGTGA CAAATGCAGC CTCGTGCGGA GCTTTTTTGT AGCAAGCTTA                                                                                    |
| 3011 | PstI                                                                                                                                                           |
|      | ~~~~~                                                                                                                                                          |
|      | M K Q F S A K H V L A V V T A G H A L A A S ·                                                                                                                  |
| 5111 | ACATGAAGCA GTTCTCCGCC AAACACGTCC TCGCAGTTGT GGTGACTGCA GGGCACGCCT TAGCAGCCTC                                                                                   |
| 2111 | TQGISEDLYSRLVEMATISQAAY                                                                                                                                        |
| 5101 | TACGCAAGGC ATCTCCGAAG ACCTCTACAG CCGTTTAGTC GAAATGGCCA CTATCTCCCA AGCTGCCTAC                                                                                   |
| 5181 | Sali                                                                                                                                                           |
|      | 2a11                                                                                                                                                           |
|      |                                                                                                                                                                |
|      | A D L C N I P S T I I K G E K I Y N S Q T D I N                                                                                                                |
| 5251 | GCCGACCTGT GCAACATTCC GTCGACTATT ATCAAGGGAG AGAAAATTTA CAATTCTCAA ACTGACATTA                                                                                   |
|      | В                                                                                                                                                              |
|      | ~                                                                                                                                                              |
|      | · G W                                                                                                                                                          |
|      | 5321 ACGGATG                                                                                                                                                   |
|      |                                                                                                                                                                |

### Figure 37 A



#### Figure 39 B

|           | NcoI                                                                                                                                                                                                                                                     |
|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|           | HindIII                                                                                                                                                                                                                                                  |
| 1         | M A H A R V L L L A V L A T A A V A V AAGCTTACCA TGGCCCACGC CCGCGTCCTC CTCCTGGCGC TCGCCGTGCT GGCCACGGCC GCCGTCGCCG                                                                                                                                       |
|           | NPIR NotI                                                                                                                                                                                                                                                |
| 71<br>141 | · A S S S S F A D S N P I R P V T D R A A A S T TCGCCTCCTC CTCCTCCTC GCCGACTCCA ACCCGATCCG GCCCGTCACC GACCGCGCGG CCGCCTCCAC · Q G I S E D L Y S R L V E M A T I S Q A A Y A GCAGGGCATC TCCGAAGACC TCTACAGCCG TTTAGTCGAA ATGGCCACTA TCTCCCAAGC TGCCTACGCC |
|           | SalI                                                                                                                                                                                                                                                     |
| 211       | D L C N I P S T I I K G E K I Y N S Q T D I N G<br>GACCTGTGCA ACATTCCGTC GACTATTATC AAGGGAGAGA AAATTTACAA TTCTCAAACT GACATTAACG                                                                                                                          |
|           | BamHI                                                                                                                                                                                                                                                    |
| 281       | · W I L R D D S S K E I I T V F R G T G S D T N GATGGATCCT CCGCGACGAC AGCAGCAAAG AAATAATCAC CGTCTTCCGT GGCACTGGTA GTGATACGAA                                                                                                                             |
|           | Glycosylation                                                                                                                                                                                                                                            |
| 351       | . L Q L D T N Y T L T P F D T L P Q C N G C E V TCTACAACTC GATACTAACT ACACCCTCAC GCCTTTCGAC ACCCTACCAC AATGCAACGG TTGTGAAGTA H G G Y Y I G W V S V Q D Q V E S L V K Q Q V S                                                                             |
| 421       | CACGGTGGAT ATTATATTGG ATGGGTCTCC GTCCAGGACC AAGTCGAGTC GCTTGTCAAA CAGCAGGTTA . Q $^{ m P}$ D $^{ m P}$ A $^{ m L}$ T $^{ m V}$ T G H X L G A S L A A L T A                                                                                               |
| 491       | GCCAGTATCC GGACTACGCG CTGACCGTGA CCGGCCACKC CCTCGGCGCC TCCCTGGCGG CACTCACTGC · A Q L S A T Y D N I R L Y T F G E P R S G N O                                                                                                                             |
| 561       | CGCCCAGCTG TCTGCGACAT ACGACAACAT CCGCCTGTAC ACCTTCGGCG AACCGCGCAG CGGCAATCAG                                                                                                                                                                             |
|           | XhoI<br>~~~~~                                                                                                                                                                                                                                            |
| 631       | A F A S Y M N D A F Q A S S P D T T Q Y F R V T<br>GCCTTCGCGT CGTACATGAA CGATGCCTTC CAAGCCTCGA GCCCAGATAC GACGCAGTAT TTCCGGGTCA                                                                                                                          |
|           | NcoI                                                                                                                                                                                                                                                     |
| 701       | · H A N D G I P N L P P V E Q G Y A H G G V E Y CTCATGCCAA CGACGCATC CCAAACCTGC CCCCGGTGGA GCAGGGGTAC GCCCATGGCG GTGTAGAGTA · W S V D P Y S A Q N T F V C T G D E V Q C C E                                                                              |
|           | . ws v D P i S A Q N T F V C T G D E V Q C C E                                                                                                                                                                                                           |

A Q G G Q G V N N A H T T Y F G M T S G A C T  $_{\rm W}$  841 GCCCAGGGCG GACAGGGTGT GAATAATGCG CACACGACTT ATTTTGGGAT GACGAGCGGC GCATGCACCT

CTGGAGCGTT GATCCTTACA GCGCCCAGAA CACATTTGTC TGCACTGGGG ATGAAGTGCA GTGCTGTGAG

SphI

## Figure 39 C

|                |                 | NotI                     |                          | KDEL         |               |                                         |            |
|----------------|-----------------|--------------------------|--------------------------|--------------|---------------|-----------------------------------------|------------|
|                |                 | ~~~~~                    |                          | ~~~~~~~~     |               |                                         |            |
| 911            | · P V A         |                          | T T E                    | _            |               |                                         |            |
| 981            | TAAACTTUCT      | GGCCGCGGAA               | ACCACTGAAG               | GATGAGCTGT   | AAAGAAGCAG    | ATCGTTCAAA                              | CATTTGGCAA |
| 1051           | THANGITICI      | TAAGATTGAA               | TCCTGTTGCC               | GGTCTTGCGA   | TGATTATCAT    | ATAATTTCTG                              | TTGAATTACG |
| 1121           |                 | AATAATTAAC               |                          |              |               |                                         |            |
| 1121           | GCAATTATAC      | ATTTAATACG               | CGATAGAAAA               | CAAAATATAG   | CGCGCAAAC'I'  | AGGATAAATT                              | ATCGCGCGCG |
|                |                 |                          | HindI                    |              |               |                                         |            |
|                |                 | (                        | ClaI                     | ~~<br>XbaI   |               |                                         |            |
|                |                 |                          | ~~~~                     | ~~~~~        |               |                                         |            |
| 1191           | GTGTCATCTA      | TGTTACTAGA               | TCGATAAGCT               | TCTAGAGCGG   | CCGGTGGAGC    | TCCAATTCGC                              | CCTATAGTGA |
| 1261           | GTCGTATTAC      | GCGCGCTCAC               | TGGCCGTCGT               | TTTACAACGT   | CGTGACTGGG    | AAAACCCTGG                              | CGTTACCCAA |
| 1331           | CTTAATCGCC      | TTGCAGCACA               | TCCCCCTTTC               | GCCAGCTGGC   | GTAATAGCGA    | AGAGGCCCGC                              | ACCGATCGCC |
| 1401           | CTTCCCAACA      | GTTGCGCAGC               | CTGAATGGCG               | AATGGGACGC   | GCCCTGTAGC    | GGCGCATTAA                              | GCGCGGCGGG |
| 1471           | TGTGGTGGTT      | ACGCGCAGCG               | TGACCGCTAC               | ACTTGCCAGC   | GCCCTAGCGC    | CCGCTCCTTT                              | CGCTTTCTTC |
| 1541           | CCTTCCTTTC      | TCGCCACGTT               | CGCCGGCTTT               | CCCCGTCAAG   | CTCTAAATCG    | GGGGCTCCCT                              | TTAGGGTTCC |
| 1611           | GATTTAGTGC      | TTTACGGCAC               | CTCGACCCCA               | AAAAACTTGA   | TTAGGGTGAT    | GGTTCACGTA                              | GTGGGCCATC |
| 1681           | GCCCTGATAG      | ACGGTTTTTC               | GCCCTTTGAC               | GTTGGAGTCC   | ACGTTCTTTA    | ATAGTGGACT                              | CTTGTTCCAA |
| 1751           | ACTGGAACAA      | CACTCAACCC               | TATCTCGGTC               | TATTCTTTTG   | ATTTATAAGG    | GATTTTGCCG                              | ATTTCGGCCT |
| 1821           | ATTGGTTAAA      | AAATGAGCTG               | ATTTAACAAA               | AATTTAACGC   | GAATTTTAAC    | AAAATATTAA                              | CGCTTACAAT |
| 1891           | TTAGGTGGCA      | CTTTTCGGGG               | AAATGTGCGC               | GGAACCCCTA   | TTTGTTTATT    | TTTCTAAATA                              | CATTCAAATA |
| 1961           | TGTATCCGCT      | CATGAGACAA               | TAACCCTGAT               | AAATGCTTCA   | ATAATATTGA    | AAAAGGAAGA                              | GTATGAGTAT |
| 2031           | TCAACATTTC      | CGTGTCGCCC               | TTATTCCCTT               | TTTTGCGGCA   | TTTTGCCTTC    | CTGTTTTTGC                              | TCACCCAGAA |
| 2101           | ACGCTGGTGA      | AAGTAAAAGA               | TGCTGAAGAT               | CAGTTGGGTG   | CACGAGTGGG    | TTACATCGAA                              | CTGGATCTCA |
| 2171           | ACAGCGGTAA      | GATCCTTGAG               | AGTTTTCGCC               | CCGAAGAACG   | TTTTCCAATG    | ATGAGCACTT                              | TTAAAGTTCT |
| 2241           | GCTATGTGGC      | GCGGTATTAT               | CCCGTATTGA               | CGCCGGGCAA   | GAGCAACTCG    | GTCGCCGCAT                              | ACACTATTCT |
| 2311           | CAGAATGACT      | TGGTTGAGTA               | CTCACCAGTC               | ACAGAAAAGC   | ATCTTACGGA    | TGGCATGACA                              | GTAAGAGAAT |
| 2381           | TATGCAGTGC      | TGCCATAACC               | ATGAGTGATA               | ACACTGCGGC   | CAACTTACTT    | CTGACAACGA                              | TCGGAGGACC |
| 2451<br>2521   | GAAGGAGCTA      | ACCGCTTTTT               | TGCACAACAT               | GGGGGATCAT   | GTAACTCGCC    | TTGATCGTTG                              | GGAACCGGAG |
| 2521           | CIGAAIGAAG      | CCATACCAAA               | CGACGAGCGT               | GACACCACGA   | TGCCTGTAGC    | AATGGCAACA                              | ACGTTGCGCA |
| 2661           | AACTATTAAC      | TGGCGAACTA               | CTTACTCTAG               | CTTCCCGGCA   | ACAATTAATA    | GACTGGATGG                              | AGGCGGATAA |
| 2731           | CACCCTCCCT      | CCACTTCTGC               | GCTCGGCCCT               | TCCGGCTGGC   | TGGTTTATTG    | CTGATAAATC                              | TGGAGCCGGT |
| 2801           | ACACCAIGGGI     | CTCGCGGTAT               | CATTGCAGCA               | CTGGGGCCAG   | ATGGTAAGCC    | CTCCCGTATC                              | GTAGTTATCT |
| 2871           | TA A CCA TITICO | GAGTCAGGCA               | ACTATGGATG               | AACGAAATAG   | ACAGATCGCT    | GAGATAGGTG                              | CCTCACTGAT |
| 2941           | THAGCAILGG      | TAACTGTCAG               | ACCAAGTTTA               | CTCATATATA   | CTTTAGATTG    | ATTTAAAACT                              | TCATTTTTAA |
| 3011           | TCCACTCACC      | TCTAGGTGAA               | GATCCTTTT                | GATAATCTCA   | TGACCAAAAT    | CCCTTAACGT                              | GAGTTTTCGT |
| 3081           | CTCCTCCTTC      | GTCAGACCCC               | A A COA COCO             | TCAAAGGATC   | TTCTTGAGAT    | CCTTTTTTC                               | TGCGCGTAAT |
| 3151           | CIGCIGCIIG      | CAAACAAAAA               | AACCACCGCT               | ACCAGCGGTG   | GTTTGTTTGC    | CGGATCAAGA                              | GCTACCAACT |
| 3221           | TAGGCCACCA      | AGGTAACTGG               | TOTOTA                   | GCGCAGATAC   | CAAATACTGT    | CCTTCTAGTG                              | TAGCCGTAGT |
| 3291           | TGCTGCCACT      | CTTCAAGAAC               | CCTCTCTTAC               | CCCCTACATA   | CCTCGCTCTG    | CTAATCCTGT                              | TACCAGTGGC |
| 3361           | CGGTCGGGCT      | GGCGATAAGT<br>GAACGGGGGG | TTCCTCCACA               | CACCCCACC    | TCAAGACGAT    | AGTTACCGGA                              | TAAGGCGCAG |
| 3431           | ACCTACAGCG      | TGAGCTATGA               | GNANGCCCCA               | CAGCCCAGCI   | 1 GGAGCGAAC   | GACCTACACC                              | GAACTGAGAT |
| 3501           | CGGCAGGGTC      | GGAACAGGAG               | ACCCCACCAC               | CCACCTTCCCGA | CCCCCARAG     | GCGGACAGGT                              | ATCCGGTAAG |
| 3571           | GTCGGGTTTTC     | GCCACCTCTG               | ACCUCACGAG<br>ACTTCACCCT | CCAPTTTTCCA  | CATTCCTTCCTTC | ACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC | TTATAGTCCT |
| 3641           | AAAACGCCAG      | CAACGCGGCC               | 1.01.1.QVQCQ1            | TCCTCCCC     | TTCCTCCTC     | AGGGGGGGGG                              | AGCCTATGGA |
| 3711           | TGCGTTATCC      | CCTGATTCTG               | TGCDTAACCC               | TATTACCCCTT  | TIGCIGGCCI    | TTTGCTCACA                              | TGTTCTTTCC |
| 3781           | CGAACGACCG      | AGCGCAGCGA               | CTCDCTCACC               | TATTACCGCC   | TITGAGTGAG    | CIGATACCGC                              | TCGCCGCAGC |
| 3851           | CCGCGCGCGTTG    | GCCGATTCAT               | TAATCCACCT               | CCCACCACA    | COUDAGCACA    | MATACGCAAA                              | CCGCCTCTCC |
| 3921           | CAACGCAATT      | AATGTGAGTT               | AGCTCACTCA               | TTAGGCACAG   | GTTTCCCGAC    | A CTTTTA TICCE                          | GCAGTGAGCG |
| - <del>-</del> |                 |                          | CICACICA                 | JJJAJOUALL   | CAGGCITIAC    | ACTITATGCT                              | TCCGGCTCGT |

## Figure 39 D

|        | 3991 | ATGTTGTGTG | GAATTGTGAG | CGGATAACAA |            | GAAACAGCTA |            | TACGCCAAGC |
|--------|------|------------|------------|------------|------------|------------|------------|------------|
|        |      |            |            |            | KpnI       |            | XhoI       |            |
|        |      |            |            |            | ~~~~       | ~~         | ~~~~~      |            |
|        | 4061 | GCGCAATTAA | CCCTCACTAA | AGGGAACAAA | AGCTGGGTAC | CGGGCCCCCC | CTCGAGGTCA | TTCATATGCT |
|        | 4131 | TGAGAAGAGA | GTCGGGATAG | TCCAAAATAA | AACAAAGGTA | AGATTACCTG | GTCAAAAGTG | AAAACATCAG |
|        | 4201 | TTAAAAGGTG | GTATAAGTAA | AATATCGGTA | ATAAAAGGTG | GCCCAAAGTG | AAATTTACTC | TTTTCTACTA |
|        | 4271 | TTATAAAAAT | TGAGGATGTT | TTGTCGGTAC | TTTGATACGT | CATTTTTGTA | TGAATTGGTT | TTTAAGTTTA |
|        | 4341 | TTCGCGATTT | GGAAATGCAT | ATCTGTATTT | GAGTCGGTTT | TTAAGTTCGT | TGCTTTTGTA | AATACAGAGG |
|        | 4411 | GATTTGTATA | AGAAATATCT | TTAAAAAACC | CATATGCTAA | TTTGACATAA | TTTTTGAGAA | TATATAAA   |
|        |      | EcoR1      | [          |            |            |            |            |            |
|        |      | ~~~~       | ~~~        |            |            |            |            |            |
|        | 4481 | TCAGGCGAAT | TCCACAATGA | ACAATAATAA | GATTAAAATA | GCTTGCCCCC | GTTGCAGCGA | TGGGTATTTT |
|        | 4551 | TTCTAGTAAA | ATAAAAGATA | AACTTAGACT | CAAAACATTT | ACAAAAACAA | CCCCTAAAGT | CCTAAAGCCC |
|        | 4621 | AAAGTGCTAT | GCACGATCCA | TAGCAAGCCC | AGCCCAACCC | AACCCAACCC | AACCCACCCC | AGTGCAGCCA |
|        | 4691 | ACTGGCAAAT | AGTCTCCACC | CCCGGCACTA | TCACCGTGAG | TTGTCCGCAC | CACCGCACGT | CTCGCAGCCA |
|        | 4761 | AAAAAAAAA  | AAGAAAGAAA | AAAAAGAAAA | AGAAAAACAG | CAGGTGGGTC | CGGGTCGTGG | GGGCCGGAAA |
|        | 4831 | AGCGAGGAGG | ATCGCGAGCA | GCGACGAGGC | CCGGCCCTCC | CTCCGCTTCC | AAAGAAACGC | CCCCCATCGC |
|        | 4901 | CACTATATAC | ATACCCCCCC | CTCTCCTCCC | ATCCCCCCAA | CCCTACCACC | ACCACCACCA | CCACCTCCTC |
|        | 4971 | CCCCCTCGCT | GCCGGACGAC | GAGCTCCTCC | CCCCTCCCCC | TCCGCCGCCG | CCGGTAACCA | CCCCGCCCCT |
|        | 5041 | CTCCTCTTTC | TTTCTCCGTT | TTTTTTTCG  | TCTCGGTCTC | GATCTTTGGC | CTTGGTAGTT | TGGGTGGGCG |
|        | 5111 | AGAGCGGCTT | CGTCGCCCAG | ATCGGTGCGC | GGGAGGGGCG | GGATCTCGCG | GCTGGCGTCT | CCGGGCGTGA |
| i.     |      | Bar        | nHI        |            |            | BglII      |            |            |
|        |      | ~~         | ~~~~       |            |            | ~~~~~      |            |            |
|        | 5181 | GTCGGCCCGG | ATCCTCGCGG | GGAATGGGGC | TCTCGGATGT | AGATCTTCTT | TCTTTCTTCT | TTTTGTGGTA |
|        | 5251 | GAATTTGAAT | CCCTCAGCAT | TGTTCATCGG | TAGTTTTTCT | TTTCATGATT | TGTGACAAAT | GCAGCCTCGT |
|        | 5321 | GCGGAGCTTT | TTTGTAGC   |            |            |            |            |            |
| te and |      |            |            |            |            |            |            |            |

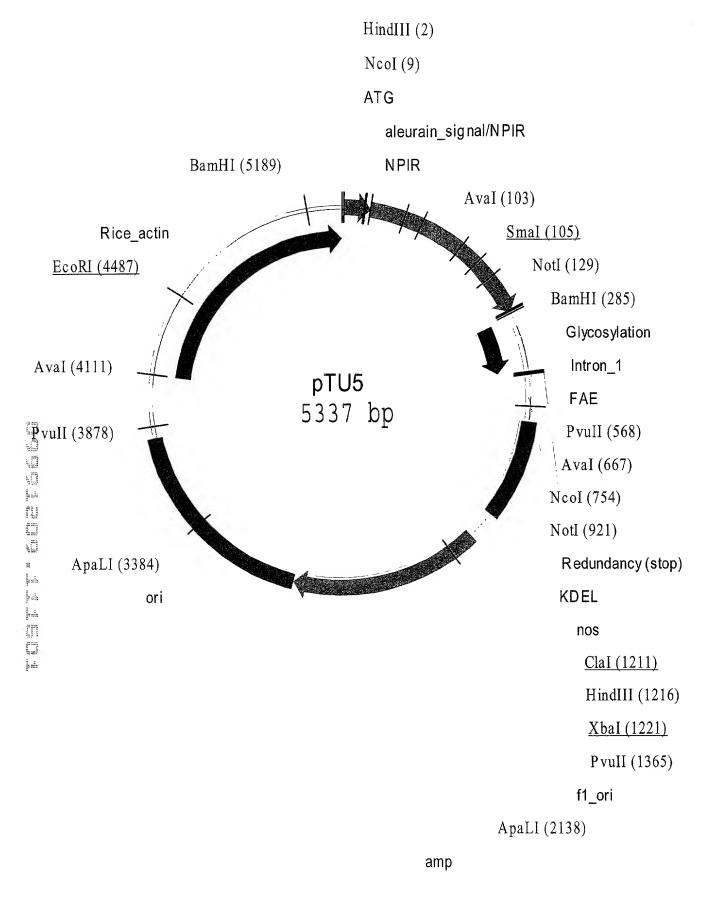


Figure 40 A

#### Sequence for pTU5

|     | HindIII No |                          |            |            |            |
|-----|------------|--------------------------|------------|------------|------------|
| 1   | AAGCTTACCA | TGGCCCACGC<br>ACCGGGTGCG |            |            |            |
| 51  |            | GCCGTCGCCG<br>CGGCAGCGGC |            |            |            |
|     | SmaI       |                          |            |            |            |
|     | AvaI       |                          | Not        |            |            |
| 101 |            | GCCCGTCACC               | GACCGCGCGG | CCGCCTCCAC |            |
|     | TGGGCCCGGC | CGGGCAGTGG               | CTGGCGCGCC | GGCGGAGGTG | CGTCCCGTAG |
| 151 |            | TCTACAGCCG               |            |            |            |
|     | AGGCTTCTGG | AGATGTCGGC               | AAATCAGCTT | TACCGGTGAT | AGAGGGTTCG |
| 201 |            | GACCTGTGCA               |            |            |            |
|     | ACGGATGCGG | CTGGACACGT               | TGTAAGGCAG | CTGATAATAG | TTCCCTCTCT |
|     |            |                          |            | BamHI      |            |
|     |            |                          |            | ~~~~~      |            |
| 251 |            | TTCTCAAACT<br>AAGAGTTTGA |            |            |            |
| 301 | AGCAGCAAAG | AAATAATCAC               | CGTCTTCCGT | GGCACTGGTA | GTGATACGAA |
| 301 |            | TTTATTAGTG               |            |            |            |
| 351 | TCTACAACTC | GATACTAACT               | ACACCCTCAC | GCCTTTCGAC | ACCCTACCAC |
|     | AGATGTTGAG | CTATGATTGA               | TGTGGGAGTG | CGGAAAGCTG | TGGGATGGTG |
| 401 |            | ; TTGTGAAGTA             |            |            |            |
|     | TTACGTTGCC | C AACACTTCAT             | GTGCCACCTA | TAATATAACC | TACCCAGAGG |
| 451 |            | : AAGTCGAGTC             |            |            |            |
|     | CAGGTCCTGG | TTCAGCTCAG               | CGAACAGTTT | GTCGTCCAAT | CGGTCATAGG |
| 501 |            | G CTGACCGTGA             |            |            |            |
|     | CCTGATGCGC | C GACTGGCACT             | GGCCGGTGMG | GGAGCCGCGG | AGGGACCGCC |
|     |            | PvuII                    |            |            |            |
| 551 | CACTCACTGO | CGCCCAGCTG               | TCTGCGACAT | ACGACAACAT | CCGCCTGTAC |
|     |            | G GCGGGTCGAC             |            |            |            |
| 601 | ACCTTCGGC  | G AACCGCGCAG             | CGGCAATCAG | GCCTTCGCGI | CGTACATGAA |
|     |            | C TTGGCGCGTC             |            |            |            |

AvaI

Fig. 40 B

|      |                          | ~~~~~                    | ~                        |                          |                          |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 651  |                          | CAAGCCTCGA<br>GTTCGGAGCT |                          |                          |                          |
| 701  |                          | CGACGGCATC<br>GCTGCCGTAG |                          |                          |                          |
|      | NcoI                     |                          |                          |                          |                          |
| 751  |                          | GTGTAGAGTA<br>CACATCTCAT |                          |                          |                          |
| 801  |                          | TGCACTGGGG<br>ACGTGACCCC |                          |                          |                          |
| 851  |                          | GAATAATGCG<br>CTTATTACGC |                          |                          |                          |
|      |                          | ~~                       | NotI                     |                          |                          |
| 901  |                          | GGCCGGTCGC<br>CCGGCCAGCG |                          |                          |                          |
| 951  | AAGAAGCAGA<br>TTCTTCGTCT | TCGTTCAAAC<br>AGCAAGTTTG |                          | AAAGTTTCTT<br>TTTCAAAGAA |                          |
| 1001 |                          | GTCTTGCGAT<br>CAGAACGCTA | GATTATCATA<br>CTAATAGTAT | TAATTTCTGT<br>ATTAAAGACA |                          |
| 1051 | TAAGCATGTA<br>ATTCGTACAT | ATAATTAACA<br>TATTAATTGT |                          | GACGTTATTT<br>CTGCAATAAA | ATGAGATGGG<br>TACTCTACCC |
| 1101 | <b>-</b>                 | TAGAGTCCCG<br>ATCTCAGGGC |                          | TTTAATACGC<br>AAATTATGCG |                          |
| 1151 |                          | GCGCAAACTA<br>CGCGTTTGAT |                          |                          | TGTCATCTAT<br>ACAGTAGATA |
|      | 111111111                |                          | XbaI                     |                          |                          |
|      | _                        | laI HindII               | ~~~~~<br>I               |                          |                          |
| 1201 | GTTACTAGAT               | CGATAAGCTT               |                          |                          | CCAATTCGCC<br>GGTTAAGCGG |
| 1251 |                          |                          |                          |                          | TTACAACGTC AATGTTGCAG    |
| 1301 |                          |                          |                          |                          | TGCAGCACAT<br>ACGTCGTGTA |
|      |                          | PvuII                    |                          |                          |                          |
| 1351 | CCCCCTTTCC               | CCAGCTGGCG               | TAATAGCGAA               | GAGGCCCGCA               | CCGATCGCCC               |

GGGGGAAAGC GGTCGACCGC ATTATCGCTT CTCCGGGCGT GGCTAGCGGG 1401 TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGGACGCG CCCTGTAGCG AAGGGTTGTC AACGCGTCGG ACTTACCGCT TACCCTGCGC GGGACATCGC 1451 GCGCATTAAG CGCGGCGGT GTGGTGGTTA CGCGCAGCGT GACCGCTACA CGCGTAATTC GCGCCGCCCA CACCACCAAT GCGCGTCGCA CTGGCGATGT 1501 CTTGCCAGCG CCCTAGCGCC CGCTCCTTTC GCTTTCTTCC CTTCCTTTCT GAACGGTCGC GGGATCGCGG GCGAGGAAAG CGAAAGAAGG GAAGGAAAGA 1551 CGCCACGTTC GCCGGCTTTC CCCGTCAAGC TCTAAATCGG GGGCTCCCTT GCGGTGCAAG CGGCCGAAAG GGGCAGTTCG AGATTTAGCC CCCGAGGGAA 1601 TAGGGTTCCG ATTTAGTGCT TTACGGCACC TCGACCCCAA AAAACTTGAT ATCCCAAGGC TAAATCACGA AATGCCGTGG AGCTGGGGTT TTTTGAACTA 1651 TAGGGTGATG GTTCACGTAG TGGGCCATCG CCCTGATAGA CGGTTTTTCG ATCCCACTAC CAAGTGCATC ACCCGGTAGC GGGACTATCT GCCAAAAAGC 1701 CCCTTTGACG TTGGAGTCCA CGTTCTTTAA TAGTGGACTC TTGTTCCAAA GGGAAACTGC AACCTCAGGT GCAAGAATT ATCACCTGAG AACAAGGTTT 1751 CTGGAACAAC ACTCAACCCT ATCTCGGTCT ATTCTTTTGA TTTATAAGGG GACCTTGTTG TGAGTTGGGA TAGAGCCAGA TAAGAAAACT AAATATTCCC 1801 ATTTTGCCGA TTTCGGCCTA TTGGTTAAAA AATGAGCTGA TTTAACAAAA TAAAACGGCT AAAGCCGGAT AACCAATTTT TTACTCGACT AAATTGTTTT 1851 ATTTAACGCG AATTTTAACA AAATATTAAC GCTTACAATT TAGGTGGCAC TAAATTGCGC TTAAAATTGT TTTATAATTG CGAATGTTAA ATCCACCGTG 1901 TTTTCGGGGA AATGTGCGCG GAACCCCTAT TTGTTTATTT TTCTAAATAC AAAAGCCCCT TTACACGCGC CTTGGGGATA AACAAATAAA AAGATTTATG 1951 ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCCTGATA AATGCTTCAA TAAGTTTATA CATAGGCGAG TACTCTGTTA TTGGGACTAT TTACGAAGTT 2001 TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC GTGTCGCCCT ATTATAACTT TTTCCTTCTC ATACTCATAA GTTGTAAAGG CACAGCGGGA 2051 TATTCCCTTT TTTGCGGCAT TTTGCCTTCC TGTTTTTGCT CACCCAGAAA ATAAGGGAAA AAACGCCGTA AAACGGAAGG ACAAAAACGA GTGGGTCTTT ApaLI 2101 CGCTGGTGAA AGTAAAAGAT GCTGAAGATC AGTTGGGTGC ACGAGTGGGT GCGACCACTT TCATTTTCTA CGACTTCTAG TCAACCCACG TGCTCACCCA 2151 TACATCGAAC TGGATCTCAA CAGCGGTAAG ATCCTTGAGA GTTTTCGCCC ATGTAGCTTG ACCTAGAGTT GTCGCCATTC TAGGAACTCT CAAAAGCGGG 2201 CGAAGAACGT TTTCCAATGA TGAGCACTTT TAAAGTTCTG CTATGTGGCG GCTTCTTGCA AAAGGTTACT ACTCGTGAAA ATTTCAAGAC GATACACCGC 2251 CGGTATTATC CCGTATTGAC GCCGGGCAAG AGCAACTCGG TCGCCGCATA GCCATAATAG GGCATAACTG CGGCCCGTTC TCGTTGAGCC AGCGGCGTAT 2301 CACTATTCTC AGAATGACTT GGTTGAGTAC TCACCAGTCA CAGAAAAGCA GTGATAAGAG TCTTACTGAA CCAACTCATG AGTGGTCAGT GTCTTTTCGT 2351 TCTTACGGAT GGCATGACAG TAAGAGAATT ATGCAGTGCT GCCATAACCA AGAATGCCTA CCGTACTGTC ATTCTCTTAA TACGTCACGA CGGTATTGGT 2401 TGAGTGATAA CACTGCGGCC AACTTACTTC TGACAACGAT CGGAGGACCG ACTCACTATT GTGACGCCGG TTGAATGAAG ACTGTTGCTA GCCTCCTGGC 2451 AAGGAGCTAA CCGCTTTTTT GCACAACATG GGGGATCATG TAACTCGCCT TTCCTCGATT GGCGAAAAAA CGTGTTGTAC CCCCTAGTAC ATTGAGCGGA 2501 TGATCGTTGG GAACCGGAGC TGAATGAAGC CATACCAAAC GACGAGCGTG ACTAGCAACC CTTGGCCTCG ACTTACTTCG GTATGGTTTG CTGCTCGCAC 2551 ACACCACGAT GCCTGTAGCA ATGGCAACAA CGTTGCGCAA ACTATTAACT TGTGGTGCTA CGGACATCGT TACCGTTGTT GCAACGCGTT TGATAATTGA 2601 GGCGAACTAC TTACTCTAGC TTCCCGGCAA CAATTAATAG ACTGGATGGA CCGCTTGATG AATGAGATCG AAGGGCCGTT GTTAATTATC TGACCTACCT 2651 GGCGGATAAA GTTGCAGGAC CACTTCTGCG CTCGGCCCTT CCGGCTGGCT CCGCCTATTT CAACGTCCTG GTGAAGACGC GAGCCGGGAA GGCCGACCGA 2701 GGTTTATTGC TGATAAATCT GGAGCCGGTG AGCGTGGGTC TCGCGGTATC CCAAATAACG ACTATTTAGA CCTCGGCCAC TCGCACCCAG AGCGCCATAG 2751 ATTGCAGCAC TGGGGCCAGA TGGTAAGCCC TCCCGTATCG TAGTTATCTA TAACGTCGTG ACCCCGGTCT ACCATTCGGG AGGGCATAGC ATCAATAGAT 2801 CACGACGGGG AGTCAGGCAA CTATGGATGA ACGAAATAGA CAGATCGCTG GTGCTGCCCC TCAGTCCGTT GATACCTACT TGCTTTATCT GTCTAGCGAC 2851 AGATAGGTGC CTCACTGATT AAGCATTGGT AACTGTCAGA CCAAGTTTAC TCTATCCACG GAGTGACTAA TTCGTAACCA TTGACAGTCT GGTTCAAATG 2901 TCATATATAC TTTAGATTGA TTTAAAACTT CATTTTTAAT TTAAAAGGAT AGTATATATG AAATCTAACT AAATTTTGAA GTAAAAATTA AATTTTCCTA 2951 CTAGGTGAAG ATCCTTTTTG ATAATCTCAT GACCAAAATC CCTTAACGTG GATCCACTTC TAGGAAAAAC TATTAGAGTA CTGGTTTTAG GGAATTGCAC 3001 AGTTTTCGTT CCACTGAGCG TCAGACCCCG TAGAAAAGAT CAAAGGATCT TCAAAAGCAA GGTGACTCGC AGTCTGGGGC ATCTTTTCTA GTTTCCTAGA 3051 TCTTGAGATC CTTTTTTCT GCGCGTAATC TGCTGCTTGC AAACAAAAAA AGAACTCTAG GAAAAAAGA CGCGCATTAG ACGACGAACG TTTGTTTTTT 3101 ACCACCGCTA CCAGCGGTGG TTTGTTTGCC GGATCAAGAG CTACCAACTC TGGTGGCGAT GGTCGCCACC AAACAAACGG CCTAGTTCTC GATGGTTGAG

Fig. 40 E

| 3151 | TTTTTCCGAA<br>AAAAAGGCTT | GGTAACTGGC<br>CCATTGACCG     | TTCAGCAGAG<br>AAGTCGTCTC | CGCAGATACC<br>GCGTCTATGG | AAATACTGTC<br>TTTATGACAG |
|------|--------------------------|------------------------------|--------------------------|--------------------------|--------------------------|
| 3201 | CTTCTAGTGT<br>GAAGATCACA |                              |                          | TTCAAGAACT<br>AAGTTCTTGA |                          |
| 3251 |                          | CTCGCTCTGC<br>GAGCGAGACG     |                          | ACCAGTGGCT<br>TGGTCACCGA |                          |
| 3301 |                          | GTGTCTTACC<br>CACAGAATGG     |                          | CAAGACGATA<br>GTTCTGCTAT |                          |
|      |                          |                              |                          | ApaLI                    |                          |
| 3351 |                          | GGTCGGGCTG<br>CCAGCCCGAC     |                          |                          |                          |
| 3401 | GGAGCGAACG<br>CCTCGCTTGC | ACCTACACCG<br>TGGATGTGGC     |                          | CCTACAGCGT<br>GGATGTCGCA |                          |
| 3451 |                          | GCTTCCCGAA<br>CGAAGGGCTT     |                          |                          |                          |
| 3501 |                          | GAACAGGAGA<br>CTTGTCCTCT     |                          |                          |                          |
| 3551 |                          | TATAGTCCTG<br>ATATCAGGAC     |                          |                          |                          |
| 3601 |                          | ATGCTCGTCA<br>TACGAGCAGT     |                          |                          | AAACGCCAGC<br>TTTGCGGTCG |
| 3651 | AACGCGGCCT<br>TTGCGCCGGA | TTTTACGGTT<br>AAAATGCCAA     |                          |                          | TTGCTCACAT<br>AACGAGTGTA |
| 3701 | GTTCTTTCCT<br>CAAGAAAGGA | GCGTTATCCC<br>CGCAATAGGG     |                          | GGATAACCGT<br>CCTATTGGCA |                          |
| 3751 |                          | TGATACCGCT ACTATGGCGA        |                          |                          |                          |
| 3801 |                          | AGGAAGCGGA<br>TCCTTCGCCT     |                          |                          |                          |
|      |                          |                              | PvuII                    |                          |                          |
| 3851 |                          | G CCGATTCATT<br>C GGCTAAGTAA | AATGCAGCTG               |                          | TTTCCCGACT<br>AAAGGGCTGA |
| 3901 |                          |                              |                          |                          | GCTCACTCAT CGAGTGAGTA    |
| 3951 | TAGGCACCC                | C AGGCTTTACA                 | CTTTATGCT                | CCGGCTCGTA               | TGTTGTGTGG               |

F: g. 40 F

ATCCGTGGGG TCCGAAATGT GAAATACGAA GGCCGAGCAT ACAACACACC 4001 AATTGTGAGC GGATAACAAT TTCACACAGG AAACAGCTAT GACCATGATT TTAACACTCG CCTATTGTTA AAGTGTGTCC TTTGTCGATA CTGGTACTAA 4051 ACGCCAAGCG CGCAATTAAC CCTCACTAAA GGGAACAAAA GCTGGGTACC TGCGGTTCGC GCGTTAATTG GGAGTGATTT CCCTTGTTTT CGACCCATGG AvaI 4101 GGGCCCCCC TCGAGGTCAT TCATATGCTT GAGAAGAGA TCGGGATAGT CCCGGGGGGG AGCTCCAGTA AGTATACGAA CTCTTCTCTC AGCCCTATCA 4151 CCAAAATAAA ACAAAGGTAA GATTACCTGG TCAAAAGTGA AAACATCAGT GGTTTTATTT TGTTTCCATT CTAATGGACC AGTTTTCACT TTTGTAGTCA 4201 TAAAAGGTGG TATAAGTAAA ATATCGGTAA TAAAAGGTGG CCCAAAGTGA ATTTTCCACC ATATTCATTT TATAGCCATT ATTTTCCACC GGGTTTCACT 4251 AATTTACTCT TTTCTACTAT TATAAAAATT GAGGATGTTT TGTCGGTACT TTAAATGAGA AAAGATGATA ATATTTTTAA CTCCTACAAA ACAGCCATGA 4301 TTGATACGTC ATTTTTGTAT GAATTGGTTT TTAAGTTTAT TCGCGATTTG AACTATGCAG TAAAAACATA CTTAACCAAA AATTCAAATA AGCGCTAAAC 4351 GAAATGCATA TCTGTATTTG AGTCGGTTTT TAAGTTCGTT GCTTTTGTAA CTTTACGTAT AGACATAAAC TCAGCCAAAA ATTCAAGCAA CGAAAACATT 4401 ATACAGAGGG ATTTGTATAA GAAATATCTT TAAAAAACCC ATATGCTAAT TATGTCTCCC TAAACATATT CTTTATAGAA ATTTTTTGGG TATACGATTA ECORI 4451 TTGACATAAT TTTTGAGAAA AATATATATT CAGGCGAATT CCACAATGAA AACTGTATTA AAAACTCTTT TTATATATAA GTCCGCTTAA GGTGTTACTT 4501 CAATAATAAG ATTAAAATAG CTTGCCCCCG TTGCAGCGAT GGGTATTTTT GTTATTATTC TAATTTTATC GAACGGGGGC AACGTCGCTA CCCATAAAAA 4551 TCTAGTAAAA TAAAAGATAA ACTTAGACTC AAAACATTTA CAAAAACAAC AGATCATTTT ATTTTCTATT TGAATCTGAG TTTTGTAAAT GTTTTTGTTG 4601 CCCTAAAGTC CTAAAGCCCA AAGTGCTATG CACGATCCAT AGCAAGCCCA GGGATTTCAG GATTTCGGGT TTCACGATAC GTGCTAGGTA TCGTTCGGGT 4651 GCCCAACCCA ACCCAACCCA ACCCACCCCA GTGCAGCCAA CTGGCAAATA CGGGTTGGGT TGGGTTGGGT CACGTCGGTT GACCGTTTAT 4701 GTCTCCACCC CCGGCACTAT CACCGTGAGT TGTCCGCACC ACCGCACGTC CAGAGGTGGG GGCCGTGATA GTGGCACTCA ACAGGCGTGG TGGCGTGCAG 4751 TCGCAGCCAA AAAAAAAAA AGAAAGAAAA AAAAGAAAAA GAAAAACAGC AGCGTCGGTT TTTTTTTTT TCTTTCTTTT TTTTCTTTTT CTTTTTGTCG

Fig. 40 G

| 4801 | AGGTGGGTCC<br>TCCACCCAGG | GGGTCGTGGG<br>CCCAGCACCC | GGCCGGAAAA<br>CCGGCCTTTT | GCGAGGAGGA<br>CGCTCCTCCT | TCGCGAGCAG<br>AGCGCTCGTC |
|------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 4851 |                          | CGGCCCTCCC<br>GCCGGGAGGG |                          | AAGAAACGCC<br>TTCTTTGCGG |                          |
| 4901 |                          | TACCCCCCCC<br>ATGGGGGGGG |                          | TCCCCCCAAC<br>AGGGGGGTTG |                          |
| 4951 |                          | CACCTCCTCC<br>GTGGAGGAGG |                          |                          | AGCTCCTCCC<br>TCGAGGAGGG |
| 5001 |                          | CCGCCGCCGC<br>GGCGGCGCG  |                          |                          | TCCTCTTTCT<br>AGGAGAAAGA |
| 5051 | TTCTCCGTTT<br>AAGAGGCAAA | TTTTTTTCGT<br>AAAAAAAGCA | CTCGGTCTCG<br>GAGCCAGAGC |                          | TTGGTAGTTT<br>AACCATCAAA |
| 5101 |                          | GAGCGGCTTC<br>CTCGCCGAAG |                          |                          |                          |
|      |                          |                          |                          |                          | mHI<br>~~~~              |
| 5151 |                          | CTGGCGTCTC<br>GACCGCAGAG |                          | TCGGCCCGGA               | TCCTCGCGGG               |
| 5201 | GAATGGGGCT<br>CTTACCCCGA | CTCGGATGTA<br>GAGCCTACAT | GATCTTCTTT<br>CTAGAAGAAA |                          | TTTGTGGTAG<br>AAACACCATC |
| 5251 |                          | CCTCAGCATT<br>GGAGTCGTAA |                          |                          | TTCATGATTT<br>AAGTACTAAA |
| 5301 |                          | CAGCCTCGTG<br>GTCGGAGCAC |                          |                          |                          |

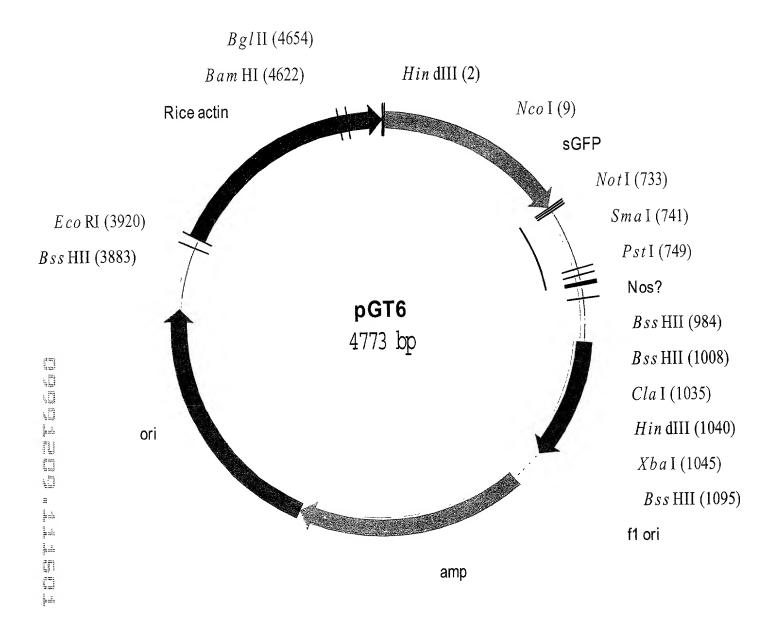


Fig. 41 A

#### Sequence for pGT6

HindIII NcoI

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- 1 AAGCTTACCA TGGTGAGCAA GGGCGAGGAG CTGTTCACCG GGGTGGTGCC CATCCTGGTC GAGCTGGACG
- TTCGAATGGT ACCACTCGTT CCCGCTCCTC GACAAGTGGC CCCACCACGG
- 71 GCGACGTGAA CGGCCACAAG TTCAGCGTGT CCGGCGAGGG CGAGGGCGAT GCCACCTACG GCAAGCTGAC
- CGCTGCACTT GCCGGTGTTC AAGTCGCACA GGCCGCTCCC GCTCCCGCTA
- 141 CCTGAAGTTC ATCTGCACCA CCGGCAAGCT GCCCGTGCCC TGGCCCACCC TCGTGACCAC CTTCACCTAC
- GGACTTCAAG TAGACGTGGT GGCCGTTCGA CGGGCACGGG ACCGGGTGGG AGCACTGGTG GAAGTGGATG
- 211 GGCGTGCAGT GCTTCAGCCG CTACCCCGAC CACATGAAGC AGCACGACTT
- CCGCACGTCA CGAAGTCGGC GATGGGGCTG GTGTACTTCG TCGTGCTGAA GAAGTTCAGG CGGTACGGGC
- 281 AAGGCTACGT CCAGGAGCGC ACCATCTTCT TCAAGGACGA CGGCAACTAC AAGACCCGCG CCGAGGTGAA
- TTCCGATGCA GGTCCTCGCG TGGTAGAAGA AGTTCCTGCT GCCGTTGATG
- 351 GTTCGAGGGC GACACCCTGG TGAACCGCAT CGAGCTGAAG GGCATCGACT TCAAGGAGGA CGGCAACATC
- ${\tt CAAGCTCCCG}~{\tt CTGTGGGACC}~{\tt ACTTGGCGTA}~{\tt GCTCGACTTC}~{\tt CCGTAGCTGA}\\ {\tt AGTTCCTCCT}~{\tt GCCGTTGTAG}$
- 421 CTGGGGCACA AGCTGGAGTA CAACTACAAC AGCCACAACG TCTATATCAT GGCCGACAAG CAGAAGAACG
- GACCCCGTGT TCGACCTCAT GTTGATGTTG TCGGTGTTGC AGATATAGTA CCGGCTGTTC GTCTTCTTGC
- 491 GCATCAAGGT GAACTTCAAG ATCCGCCACA ACATCGAGGA CGGCAGCGTG CAGCTCGCCG ACCACTACCA
- CGTAGTTCCA CTTGAAGTTC TAGGCGGTGT TGTAGCTCCT GCCGTCGCAC GTCGAGCGGC TGGTGATGGT
- 561 GCAGAACACC CCCATCGGCG ACGGCCCCGT GCTGCTGCCC GACAACCACT ACCTGAGCAC CCAGTCCGCC
- CGTCTTGTGG GGGTAGCCGC TGCCGGGGCA CGACGACGGG CTGTTGGTGA TGGACTCGTG GGTCAGGCGG
- 631 CTGAGCAAAG ACCCCAACGA GAAGCGCGAT CACATGGTCC TGCTGGAGTT CGTGACCGCC GCCGGGATCA
- GACTCGTTTC TGGGGTTGCT CTTCGCGCTA GTGTACCAGG ACGACCTCAA GCACTGGCGG CGGCCCTAGT

NotI PstI

701 CTCACGGCAT GGACGAGCTG TACAAGTAAA GCGGCCGCCC GGGCTGCAGG GAAACCACTG AAGGATGAGC

GAGTGCCGTA CCTGCTCGAC ATGTTCATTT CGCCGGCGGG CCCGACGTCC

771 TGTAAAGAAG CAGATCGTTC AAACATTTGG CAATAAAGTT TCTTAAGATT GAATCCTGTT GCCGGTCTTG

ACATTTCTTC GTCTAGCAAG TTTGTAAACC GTTATTTCAA AGAATTCTAA

841 CGATGATTAT CATATAATTT CTGTTGAATT ACGTTAAGCA TGTAATAATT AACATGTAAT GCATGACGTT

GCTACTAATA GTATATTAAA GACAACTTAA TGCAATTCGT ACATTATTAA TTGTACATTA CGTACTGCAA

911 ATTTATGAGA TGGGTTTTTA TGATTAGAGT CCCGCAATTA TACATTTAAT ACGCGATAGA AAACAAAATA

TAAATACTCT ACCCAAAAAT ACTAATCTCA GGGCGTTAAT ATGTAAATTA TGCGCTATCT TTTGTTTTAT

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981 TAGCGCGCAA ACTAGGATAA ATTATCGCGC GCGGTGTCAT CTATGTTACT AGATCGATAA GCTTCTAGAG

ATCGCGCGTT TGATCCTATT TAATAGCGCG CGCCACAGTA GATACAATGA TCTAGCTATT CGAAGATCTC

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1051 CGGCCGGTGG AGCTCCAATT CGCCCTATAG TGAGTCGTAT TACGCGCGCTCACTGGCCGT CGTTTTACAA

GCCGGCCACC TCGAGGTTAA GCGGGATATC ACTCAGCATA ATGCGCGCGA GTGACCGGCA GCAAAATGTT

1121 CGTCGTGACT GGGAAAACCC TGGCGTTACC CAACTTAATC GCCTTGCAGC ACATCCCCCT TTCGCCAGCT

1191 GGCGTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCCA ACAGTTGCGC AGCCTGAATG GCGAATGGGA

CCGCATTATC GCTTCTCCGG GCGTGGCTAG CGGGAAGGGT TGTCAACGCG TCGGACTTAC CGCTTACCCT

Fig. 41C

- 1261 CGCGCCCTGT AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGCGCA GCGTGACCGC TACACTTGCC
- GCGCGGGACA TCGCCGCGTA ATTCGCGCCG CCCACACCAC CAATGCGCGT CGCACTGGCG ATGTGAACGG
- $1331\,$  AGCGCCCTAG CGCCCGCTCC TTTCGCTTTC TTCCCTTCCT TTCTCGCCAC GTTCGCCGGC TTTCCCCGTC
- TCGCGGGATC GCGGGCGAGG AAAGCGAAAG AAGGGAAGGA AAGAGCGGTG
- 1401 AAGCTCTAAA TCGGGGGCTC CCTTTAGGGT TCCGATTTAG TGCTTTACGG CACCTCGACC CCAAAAAACT
- TTCGAGATTT AGCCCCCGAG GGAAATCCCA AGGCTAAATC ACGAAATGCC GTGGAGCTGG GGTTTTTTGA
- 1471 TGATTAGGGT GATGGTTCAC GTAGTGGGCC ATCGCCCTGA TAGACGGTTT TTCGCCCTTT GACGTTGGAG
- ACTAATCCCA CTACCAAGTG CATCACCCGG TAGCGGGACT ATCTGCCAAA
  AAGCGGGAAA CTGCAACCTC
- 1541 TCCACGTTCT TTAATAGTGG ACTCTTGTTC CAAACTGGAA CAACACTCAA CCCTATCTCG GTCTATTCTT
- AGGTGCAAGA AATTATCACC TGAGAACAAG GTTTGACCTT GTTGTGAGTT GGGATAGAGC CAGATAAGAA
- 1611 TTGATTTATA AGGGATTTTG CCGATTTCGG CCTATTGGTT AAAAAATGAG
- AACTAAATAT TCCCTAAAAC GGCTAAAGCC GGATAACCAA TTTTTTACTC GACTAAATTG TTTTTAAATT
- 1681 CGCGAATTTT AACAAAATAT TAACGCTTAC AATTTAGGTG GCACTTTTCG GGGAAATGTG CGCGGAACCC
- GCGCTTAAAA TTGTTTTATA ATTGCGAATG TTAAATCCAC CGTGAAAAGC
- 1751 CTATTTGTTT ATTTTTCTAA ATACATTCAA ATATGTATCC GCTCATGAGA CAATAACCCT GATAAATGCT
- GATAAACAAA TAAAAAGATT TATGTAAGTT TATACATAGG CGAGTACTCT GTTATTGGGA CTATTTACGA
- 1821 TCAATAATAT TGAAAAAGGA AGAGTATGAG TATTCAACAT TTCCGTGTCG
- AGTTATTATA ACTTTTTCCT TCTCATACTC ATAAGTTGTA AAGGCACAGC
- 1891 GCATTTTGCC TTCCTGTTTT TGCTCACCCA GAAACGCTGG TGAAAGTAAA AGATGCTGAA GATCAGTTGG
- CGTAAAACGG AAGGACAAAA ACGAGTGGGT CTTTGCGACC ACTTTCATTT
- 1961 GTGCACGAGT GGGTTACATC GAACTGGATC TCAACAGCGG TAAGATCCTT GAGAGTTTTC GCCCCGAAGA

CACGTGCTCA CCCAATGTAG CTTGACCTAG AGTTGTCGCC ATTCTAGGAA

2031 ACGTTTCCA ATGATGAGCA CTTTTAAAGT TCTGCTATGT GGCGCGGTAT TATCCCGTAT TGACGCCGGG

TGCAAAAGGT TACTACTCGT GAAAATTTCA AGACGATACA CCGCGCCATA ATAGGGCATA ACTGCGGCCC

2101 CAAGAGCAAC TCGGTCGCCG CATACACTAT TCTCAGAATG ACTTGGTTGA GTACTCACCA GTCACAGAAA

GTTCTCGTTG AGCCAGCGGC GTATGTGATA AGAGTCTTAC TGAACCAACT CATGAGTGGT CAGTGTCTTT

2171 AGCATCTTAC GGATGGCATG ACAGTAAGAG AATTATGCAG TGCTGCCATA ACCATGAGTG ATAACACTGC

TCGTAGAATG CCTACCGTAC TGTCATTCTC TTAATACGTC ACGACGGTAT TGGTACTCAC TATTGTGACG

2241 GGCCAACTTA CTTCTGACAA CGATCGGAGG ACCGAAGGAG CTAACCGCTT TTTTGCACAA CATGGGGGAT

CCGGTTGAAT GAAGACTGTT GCTAGCCTCC TGGCTTCCTC GATTGGCGAA
AAAACGTGTT GTACCCCCTA

2311 CATGTAACTC GCCTTGATCG TTGGGAACCG GAGCTGAATG AAGCCATACC AAACGACGAG CGTGACACCA

 ${\tt GTACATTGAG} \ {\tt CGGAACTAGC} \ {\tt AACCCTTGGC} \ {\tt CTCGACTTAC} \ {\tt TTCGGTATGG} \\ {\tt TTTGCTGCTC} \ {\tt GCACTGTGGT} \\$ 

2381 CGATGCCTGT AGCAATGGCA ACAACGTTGC GCAAACTATT AACTGGCGAA

GCTACGGACA TCGTTACCGT TGTTGCAACG CGTTTGATAA TTGACCGCTTGATGAATGAG ATCGAAGGGC

2451 GCAACAATTA ATAGACTGGA TGGAGGCGGA TAAAGTTGCA GGACCACTTC TGCGCTCGGC CCTTCCGGCT

CGTTGTTAAT TATCTGACCT ACCTCCGCCT ATTTCAACGT CCTGGTGAAG ACGCGAGCCG GGAAGGCCGA

 $2521\,$  GGCTGGTTTA TTGCTGATAA ATCTGGAGCC GGTGAGCGTG GGTCTCGCGG TATCATTGCA GCACTGGGGC

CCGACCAAAT AACGACTATT TAGACCTCGG CCACTCGCAC CCAGAGCGCC ATAGTAACGT CGTGACCCCG

2591 CAGATGGTAA GCCCTCCCGT ATCGTAGTTA TCTACACGAC GGGGAGTCAG GCAACTATGG ATGAACGAAA

 ${\tt GTCTACCATT~CGGGAGGGCA~TAGCATCAAT~AGATGTGCTG~CCCTCAGTC}\\ {\tt CGTTGATACC~TACTTGCTTT}$ 

2661 TAGACAGATC GCTGAGATAG GTGCCTCACT GATTAAGCAT TGGTAACTGT CAGACCAAGT TTACTCATAT

ATCTGTCTAG CGACTCTATC CACGGAGTGA CTAATTCGTA ACCATTGACA

2731 ATACTTTAGA TTGATTTAAA ACTTCATTTT TAATTTAAAA GGATCTAGGT GAAGATCCTT TTTGATAATC

TATGAAATCT AACTAAATTT TGAAGTAAAA ATTAAATTTT CCTAGATCCA

2801 TCATGACCAA AATCCCTTAA CGTGAGTTTT CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG

AGTACTGGTT TTAGGGAATT GCACTCAAAA GCAAGGTGAC TCGCAGTCTG

2871 ATCTTCTTGA GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG

TAGAAGAACT CTAGGAAAAA AAGACGCGCA TTAGACGACG AACGTTTGTT

2941 GTGGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC AGAGCGCAGA

CACCAAACAA ACGGCCTAGT TCTCGATGGT TGAGAAAAAG GCTTCCATTG

3011 TACCAAATAC TGTCCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG AACTCTGTAG CACCGCCTAC

ATGGTTTATG ACAGGAAGAT CACATCGGCA TCAATCCGGT GGTGAAGTTC

3081 ATACCTCGCT CTGCTAATCC TGTTACCAGT GGCTGCTGCC AGTGGCGATA AGTCGTGTCT TACCGGGTTG

TATGGAGCGA GACGATTAGG ACAATGGTCA CCGACGACGG TCACCGCTAT TCAGCACAGA ATGGCCCAAC

3151 GACTCAAGAC GATAGTTACC GGATAAGGCG CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA

CTGAGTTCTG CTATCAATGG CCTATTCCGC GTCGCCAGCC CGACTTGCCC CCCAAGCACG TGTGTCGGGT

3221 GCTTGGAGCG AACGACCTAC ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC

CGAACCTCGC TTGCTGGATG TGGCTTGACT CTATGGATGT CGCACTCGAT ACTCTTTCGC GGTGCGAAGG

3291 CGAAGGGAGA AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC GAGGGAGCTT

 ${\tt GCTTCCCTCT\ TTCCGCCTGT\ CCATAGGCCA\ TTCGCCGTCC\ CAGCCTTGTC\ CTCTCGCGTG\ CTCCCTCGAA}$ 

3361 CCAGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCGGGT TTCGCCACCT

 ${\tt GGTCCCCCTT\ TGCGGACCAT\ AGAAATATCA\ GGACAGCCCA\ AAGCGGTGGA} \\ {\tt GACTGAACTC\ GCAGCTAAAA}$ 

3431 TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG GCCTTTTTAC GGTTCCTGGC

ACACTACGAG CAGTCCCCCC GCCTCGGATA CCTTTTTGCG GTCGTTGCGC

 $3\,501$  CTTTTGCTG CCTTTTGCTC ACATGTTCTT TCCTGCGTTA TCCCCTGATT CTGTGGATAA CCGTATTACC

GAAAACGACC GGAAAACGAG TGTACAAGAA AGGACGCAAT AGGGGACTAA GACACCTATT GGCATAATGG

3571 GCCTTTGAGT GAGCTGATAC CGCTCGCCGC AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG

3641 CGGAAGAGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG TTGGCCGATT CATTAATGCA GCTGGCACGA

GCCTTCTCGC GGGTTATGCG TTTGGCGGAG AGGGGCGCGC AACCGGCTAA

3711 CAGGTTTCCC GACTGGAAAG CGGGCAGTGA GCGCAACGCA ATTAATGTGA GTTAGCTCAC TCATTAGGCA

GTCCAAAGGG CTGACCTTTC GCCCGTCACT CGCGTTGCGT TAATTACACT CAATCGAGTG AGTAATCCGT

3781 CCCCAGGCTT TACACTTTAT GCTTCCGGCT CGTATGTTGT GTGGAATTGT GAGCGGATAA CAATTTCACA

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3851 CAGGAAACAG CTATGACCAT GATTACGCCA AGCGCGCAAT TAACCCTCAC TAAAGGGAAC AAAAGCTGGA

 ${\tt GTCCTTGTC} \ \ {\tt GATACTGGTA} \ \ {\tt CTAATGCGGT} \ \ {\tt TCGCGCGTTA} \ \ {\tt ATTGGGAGTG}$   ${\tt ATTTCCCTTG} \ \ {\tt TTTTCGACCT}$ 

EcoRI

\_\_\_\_

3921 ATTCCACAAT GAACAATAAT AAGATTAAAA TAGCTTGCCC CCGTTGCAGC GATGGGTATT TTTTCTAGTA

TAAGGTGTTA CTTGTTATTA TTCTAATTTT ATCGAACGGG GGCAACGTCG

3991 AAATAAAAGA TAAACTTAGA CTCAAAACAT TTACAAAAAC AACCCCTAAA GTCCTAAAGC CCAAAGTGCT

TTTATTTCT ATTTGAATCT GAGTTTTGTA AATGTTTTTG TTGGGGATTT CAGGATTTCG GGTTTCACGA

4131 ATAGTCTCCA CCCCCGGCAC TATCACCGTG AGTTGTCCGC ACCACCGCAC GTCTCGCAGC CAAAAAAAAA

TATCAGAGGT GGGGGCCGTG ATAGTGGCAC TCAACAGGCG TGGTGGCGTG CAGAGCGTCG GTTTTTTTTT

4201 AAAAGAAAGA AAAAAAAGAA AAAGAAAAAC AGCAGGTGGG TCCGGGTCGT

4271 GGATCGCGAG CAGCGACGAG GCCCGGCCCT CCCTCCGCTT CCAAAGAAAC GCCCCCCATC GCCACTATAT

CCTAGCGCTC GTCGCTGCTC CGGGCCGGGA GGGAGGCGAA GGTTTCTTTG

4341 ACATACCCCC CCCTCTCCTC CCATCCCCCC AACCCTACCA CCACCACCAC CACCACCTCC TCCCCCCTCG

TGTATGGGGG GGGAGAGGAG GGTAGGGGGG TTGGGATGGT GGTGGTGGTG

4411 CTGCCGGACG ACGAGCTCCT CCCCCCTCCC CCTCCGCCGC CGCCGGTAAC CACCCCGCCC CTCTCCTCTT

GACGGCCTGC TGCTCGAGGA GGGGGGAGGG GGAGGCGGCG GCGGCCATTG

4481 TCTTTCTCCG TTTTTTTTT CGTCTCGGTC TCGATCTTTG GCCTTGGTAG TTTGGGTGGG CGAGAGCGGC

AGAAAGAGGC AAAAAAAAA GCAGAGCCAG AGCTAGAAAC CGGAACCATC AAACCCACCC GCTCTCGCCG

4551 TTCGTCGCCC AGATCGGTGC GCGGGAGGGG CGGGATCTCG CGGCTGGCGT

AAGCAGCGGG TCTAGCCACG CGCCCTCCCC GCCCTAGAGC GCCGACCGCA GAGGCCCGCA CTCAGCCGGG

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4621 GGATCCTCGC GGGGAATGGG GCTCTCGGAT GTAGATCTTC TTTCTTTCTT

CCTAGGAGCG CCCCTTACCC CGAGAGCCTA CATCTAGAAG AAAGAAAGAA GAAAAAACACC ATCTTAAACT

4691 ATCCCTCAGC ATTGTTCATC GGTAGTTTTT CTTTTCATGA TTTGTGACAA ATGCAGCCTC GTGCGGAGCT

TAGGGAGTCG TAACAAGTAG CCATCAAAAA GAAAAGTACT AAACACTGTT TACGTCGGAG CACGCCTCGA

4761 TTTTTGTAGG TAG
AAAAACATCC ATC

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### Sequence for pJQ5

NcoI

~~~~ KpnI

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 $_{\rm 1}$  CATGGGCCAG GTATAATTAT GGGATATCTC AAGCAAATAA TCGAAATATC ACCATTGGCT ACAATATCTG

 ${\tt GTACCCGGTC} \ \ {\tt CATATTAATA} \ \ {\tt CCCTATAGAG} \ \ {\tt TTCGTTTATT} \ \ {\tt AGCTTTATAG} \\ {\tt TGGTAACCGA} \ \ {\tt TGTTATAGAC} \\$ 

PstI XbaI XbaI

71 AGCTCCGAGT TCTGACTGCA GTCTGGATGA CGCGTGTTGT ATCTAGAACT CTAGATAGCA CAGCCACAGC

TCGAGGCTCA AGACTGACGT CAGACCTACT GCGCACAACA TAGATCTTGA

 $141\,$  ACCTACAGGA GTGCGACACT TGTGGACTGT AGTAGTGTTG GAGACGGAGC TCTTTCCTAC CTCCTGACGT

211 TGCCGCCGTT GTCCATTCCA ACGGCATCAC TCTCAACCAA TCACGCGCTC CCAACAAAAT ATCGTCCCCC

ACGGCGGCAA CAGGTAAGGT TGCCGTAGTG AGAGTTGGTT AGTGCGCGAG

281 ATGTCTTGGC GGAGAGAGA TACATACATG CTGTCGCGCC GTTTTTGTCT GAATCTCGCT TCCACTGGCC

TACAGAACCG CCTCTCTCTC ATGTATGTAC GACAGCGCGG CAAAAACAGA

SmaI

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 $351\,$  AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA

 ${\tt TTAGTCGAGT\ CGAGGGCCCT\ CGAGTGAGTA\ AGTTCTAGGG\ TAGCAGCAGC\ AGTGGGGACC\ GCAGTACCCT}$ 

421 TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT

 ${\tt ACCTTTCTT~GGAGGCAACG~AGCCTACTCA~GTCGGTATAG~GGGCTTGTCT}\\ {\tt CATGACGTTC~TATTGGGTTA}$ 

SphI

~~~~

491 TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG

AGTCTAAGGG GGTTATCTCT TTCATATCGT ACGAAAGCCC AAAACAAACC
GAATTAACTG AAATAAAAAC

561 TTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG

AACCTCAACT TACGACTAAA CAACACATTT TACGGGTTGG TAGACTTATA

631 CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT

GATTAATTAA ATATCGTTCT AAGACATCAC GTGTAGCGTT TATAGAAAGA CCCGTAATGT CGACCTCCGA

### PstI

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701 TCATCAGCCT GAAACACTCT GCAGAGCCTG AAGCAAGTGG TGAAGCGTGG CGATGAGATG GGTATAAAAC

AGTAGTCGGA CTTTGTGAGA CGTCTCGGAC TTCGTTCACC ACTTCGCACC GCTACTCTAC CCATATTTTG

841 GTAAAATACT GTTGCCCACT CGCCGGCGAG ATGGMCGTGC ACAAGGAGGT SAACTTCGTS GCCTACCTCC

CATTTATGA CAACGGGTGA GCGGCCGCTC TACCKGCACG TGTTCCTCCA STTGAAGCAS CGGATGGAGG

### NcoI

911 TGATCGTSCT CGGCCTCCTC TTGCTCGTST CCGCCATGGA GCACGTGGAC GCCAAGGCCT GCACCCKCGA

ACTAGCASGA GCCGGAGGAG AACGAGCASA GGCGGTACCT CGTGCACCTG

### NotI

981 GTGCGGCAAC CTCGGCTTCG GCATCTGCCC GGCGGCCGCC TCCACGCAGG

CACGCCGTTG GAGCCGAAGC CGTAGACGGG CCGCCGGCGG AGGTGCGTCC CGTAGAGGCT TCTGGAGATG

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Call

AccI

1051 AGCCGTTTAG TCGAAATGGC CACTATCTCC CAAGCTGCCT ACGCCGACCT GTGCAACATT CCGTCGACTA

TCGGCAAATC AGCTTTACCG GTGATAGAGG GTTCGACGGA TGCGGCTGGA CACGTTGTAA GGCAGCTGAT

Fig. 42 C

1121 TTATCAAGGG AGAGAAAATT TACAATTCTC AAACTGACAT TAACGGATGG ATCCTCCGCG ACGACAGCAG

AATAGTTCCC TCTCTTTTAA ATGTTAAGAG TTTGACTGTA ATTGCCTACC TAGGAGGCGC TGCTGTCGTC

- 1191 CAAAGAATA ATCACCGTCT TCCGTGGCAC TGGTAGTGAT ACGAATCTAC AACTCGATAC TAACTACACC
- GTTTCTTTAT TAGTGGCAGA AGGCACCGTG ACCATCACTA TGCTTAGATG
- 1261 CTCACGCCTT TCGACACCCT ACCACAATGC AACGGTTGTG AAGTACACGG TGGATATTAT ATTGGATGGG

GAGTGCGGAA AGCTGTGGGA TGGTGTTACG TTGCCAACAC TTCATGTGCC ACCTATAATA TAACCTACCC

1331 TCTCCGTCCA GGACCAAGTC GAGTCGCTTG TCAAACAGCA GGTTAGCCAG TATCCGGACT ACGCGCTGAC

 ${\tt AGAGGCAGGT\ CCTGGTTCAG\ CTCAGCGAAC\ AGTTTGTCGT\ CCAATCGGTC\ ATAGGCCTGA\ TGCGCGACTG}$ 

1401 CGTGACCGGC CACKCCCTCG GCGCCTCCCT GGCGGCACTC ACTGCCGCCC AGCTGTCTGC GACATACGAC

GCACTGGCCG GTGMGGGAGC CGCGGAGGGA CCGCCGTGAG TGACGGCGGG
TCGACAGACG CTGTATGCTG

1471 AACATCCGCC TGTACACCTT CGGCGAACCG CGCAGCGGCA ATCAGGCCTT CGCGTCGTAC ATGAACGATG

TTGTAGGCGG ACATGTGGAA GCCGCTTGGC GCGTCGCCGT TAGTCCGGAA GCGCAGCATG TACTTGCTAC

### XhoI

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1541 CCTTCCAAGC CTCGAGCCCA GATACGACGC AGTATTTCCG GGTCACTCAT GCCAACGACG GCATCCCAAA

GGAAGGTTCG GAGCTCGGGT CTATGCTGCG TCATAAAGGC CCAGTGAGTA

### NcoI

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- 1611 CCTGCCCCG GTGGAGCAGG GGTACGCCCA TGGCGGTGTA GAGTACTGGA GCGTTGATCC TTACAGCGCC
- GGACGGGGC CACCTCGTCC CCATGCGGGT ACCGCCACAT CTCATGACCT CGCAACTAGG AATGTCGCGG
- 1681 CAGAACACAT TTGTCTGCAC TGGGGATGAA GTGCAGTGCT GTGAGGCCCA GGGCGGACAG GGTGTGAATA
- GTCTTGTGTA AACAGACGTG ACCCCTACTT CACGTCACGA CACTCCGGGT
- 1751 ATGCGCACAC GACTTATTTT GGGATGACGA GCGGAGCCTG TACATGGTGA TCAGTCATTT CAGCCTCCCC

TACGCGTGTG CTGAATAAAA CCCTACTGCT CGCCTCGGAC ATGTACCACT AGTCAGTAAA GTCGGAGGGG

1821 GAGTGTACCA GGAAAGATGG ATGTCCTGGA GAGGGGGCCG CGTAACCACT GAAGGATGAG CTGTAAAGAA

CTCACATGGT CCTTTCTACC TACAGGACCT CTCCCCCGGC GCATTGGTGA

1891 GCAGATCGTT CAAACATTTG GCAATAAAGT TTCTTAAGAT TGAATCCTGT TGCCGGTCTT GCGATGATTA

CGTCTAGCAA GTTTGTAAAC CGTTATTTCA AAGAATTCTA ACTTAGGACA
ACGGCCAGAA CGCTACTAAT

1961 TCATATAATT TCTGTTGAAT TACGTTAAGC ATGTAATAAT TAACATGTAA TGCATGACGT TATTTATGAG

AGTATATTAA AGACAACTTA ATGCAATTCG TACATTATTA ATTGTACATT ACGTACTGCA ATAAATACTC

BssHII

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2031 ATGGGTTTTT ATGATTAGAG TCCCGCAATT ATACATTTAA TACGCGATAG AAAACAAAAT ATAGCGCGCA

TACCCAAAAA TACTAATCTC AGGGCGTTAA TATGTAAATT ATGCGCTATC

XbaI

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BssHII

ClaI HindIII

2101 AACTAGGATA AATTATCGCG CGCGGTGTCA TCTATGTTAC TAGATCGATA AGCTTCTAGA GCGGCCGGTG

TTGATCCTAT TTAATAGCGC GCGCCACAGT AGATACAATG ATCTAGCTAT TCGAAGATCT CGCCGGCCAC

#### BssHII

2171 GAGCTCCAAT TCGCCCTATA GTGAGTCGTA TTACGCGCGC TCACTGGCCG TCGTTTTACA ACGTCGTGAC

CTCGAGGTTA AGCGGGATAT CACTCAGCAT AATGCGCGCG AGTGACCGGC AGCAAAATGT TGCAGCACTG

2241 TGGGAAAACC CTGGCGTTAC CCAACTTAAT CGCCTTGCAG CACATCCCCC TTTCGCCAGC TGGCGTAATA

ACCCTTTTGG GACCGCAATG GGTTGAATTA GCGGAACGTC GTGTAGGGGG AAAGCGGTCG ACCGCATTAT

2311 GCGAAGAGGC CCGCACCGAT CGCCCTTCCC AACAGTTGCG CAGCCTGAAT GGCGAATGGG ACGCGCCCTG

CGCTTCTCCG GGCGTGGCTA GCGGGAAGGG TTGTCAACGC GTCGGACTTA

- 2381 TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTTACGCGC AGCGTGACCG CTACACTTGC CAGCGCCCTA
- ATCGCCGCGT AATTCGCGCC GCCCACACCA CCAATGCGCG TCGCACTGGC GATGTGAACG GTCGCGGGAT
- 2451 GCGCCCGCTC CTTTCGCTTT CTTCCCTTCC TTTCTCGCCA CGTTCGCCGG
- CGCGGGCGAG GAAAGCGAAA GAAGGGAAGG AAAGAGCGGT GCAAGCGGCC GAAAGGGGCA GTTCGAGATT
- 2521 ATCGGGGGCT CCCTTTAGGG TTCCGATTTA GTGCTTTACG GCACCTCGAC CCCAAAAAAC TTGATTAGGG
- TAGCCCCGA GGGAAATCCC AAGGCTAAAT CACGAAATGC CGTGGAGCTG
- 2591 TGATGGTTCA CGTAGTGGGC CATCGCCCTG ATAGACGGTT TTTCGCCCTT TGACGTTGGA GTCCACGTTC
- ACTACCAAGT GCATCACCCG GTAGCGGGAC TATCTGCCAA AAAGCGGGAA ACTGCAACCT CAGGTGCAAG
- 2661 TTTAATAGTG GACTCTTGTT CCAAACTGGA ACAACACTCA ACCCTATCTC GGTCTATTCT TTTGATTTAT
- AAATTATCAC CTGAGAACAA GGTTTGACCT TGTTGTGAGT TGGGATAGAG CCAGATAAGA AAACTAAATA
- 2731 AAGGGATTTT GCCGATTTCG GCCTATTGGT TAAAAAATGA GCTGATTTAA CAAAAATTTA ACGCGAATTT
- TTCCCTAAAA CGGCTAAAGC CGGATAACCA ATTTTTTACT CGACTAAATT GTTTTTAAAT TGCGCTTAAA
- 2801 TAACAAAATA TTAACGCTTA CAATTTAGGT GGCACTTTTC GGGGAAATGT GCGCGGAACC CCTATTTGTT
- ATTGTTTTAT AATTGCGAAT GTTAAATCCA CCGTGAAAAG CCCCTTTACA CGCGCCTTGG GGATAAACAA
- 2871 TATTTTCTA AATACATTCA AATATGTATC CGCTCATGAG ACAATAACCC TGATAAATGC TTCAATAATA
- ATAAAAAGAT TTATGTAAGT TTATACATAG GCGAGTACTC TGTTATTGGG ACTATTACG AAGTTATTAT
- 2941 TTGAAAAAGG AAGAGTATGA GTATTCAACA TTTCCGTGTC GCCCTTATTC CCTTTTTTGC GGCATTTTGC
- AACTTTTTCC TTCTCATACT CATAAGTTGT AAAGGCACAG CGGGAATAAG GGAAAAAACG CCGTAAAACG
- 3011 CTTCCTGTTT TTGCTCACCC AGAAACGCTG GTGAAAGTAA AAGATGCTGA AGATCAGTTG GGTGCACGAG
- GAAGGACAAA AACGAGTGGG TCTTTGCGAC CACTTTCATT TTCTACGACT TCTAGTCAAC CCACGTGCTC
- 3081 TGGGTTACAT CGAACTGGAT CTCAACAGCG GTAAGATCCT TGAGAGTTTT CGCCCGAAG AACGTTTTCC

ACCCAATGTA GCTTGACCTA GAGTTGTCGC CATTCTAGGA ACTCTCAAAA GCGGGGCTTC TTGCAAAAGG

3151 AATGATGAGC ACTTTTAAAG TTCTGCTATG TGGCGCGGTA TTATCCCGTA

TTACTACTCG TGAAAATTTC AAGACGATAC ACCGCGCCAT AATAGGGCAT AACTGCGGCC CGTTCTCGTT

 $3\,2\,2\,1$  CTCGGTCGCC GCATACACTA TTCTCAGAAT GACTTGGTTG AGTACTCACC AGTCACAGAA AAGCATCTTA

GAGCCAGCGG CGTATGTGAT AAGAGTCTTA CTGAACCAAC TCATGAGTGG TCAGTGTCTT TTCGTAGAAT

- 3291 CGGATGGCAT GACAGTAAGA GAATTATGCA GTGCTGCCAT AACCATGAGT GATAACACTG CGGCCAACTT
- GCCTACCGTA CTGTCATTCT CTTAATACGT CACGACGGTA TTGGTACTCA
- 3361 ACTTCTGACA ACGATCGGAG GACCGAAGGA GCTAACCGCT TTTTTGCACA ACATGGGGGA TCATGTAACT

TGAAGACTGT TGCTAGCCTC CTGGCTTCCT CGATTGGCGA AAAAACGTGT TGTACCCCCT AGTACATTGA

- 3431 CGCCTTGATC GTTGGGAACC GGAGCTGAAT GAAGCCATAC CAAACGACGA GCGTGACACC ACGATGCCTG
- GCGGAACTAG CAACCCTTGG CCTCGACTTA CTTCGGTATG GTTTGCTGCT
- 3501 TAGCAATGGC AACAACGTTG CGCAAACTAT TAACTGGCGA ACTACTTACT CTAGCTTCCC GGCAACAATT
- ATCGTTACCG TTGTTGCAAC GCGTTTGATA ATTGACCGCT TGATGAATGA
- 3571 AATAGACTGG ATGGAGGCGG ATAAAGTTGC AGGACCACTT CTGCGCTCGG CCCTTCCGGC TGGCTGGTTT

TTATCTGACC TACCTCCGCC TATTTCAACG TCCTGGTGAA GACGCGAGCC GGGAAGGCCG ACCGACCAAA

- 3641 ATTGCTGATA AATCTGGAGC CGGTGAGCGT GGGTCTCGCG GTATCATTGC AGCACTGGGG CCAGATGGTA
- TAACGACTAT TTAGACCTCG GCCACTCGCA CCCAGAGCGC CATAGTAACG
- 3711 AGCCCTCCCG TATCGTAGTT ATCTACACGA CGGGGAGTCA GGCAACTATG GATGAACGAA ATAGACAGAT

 ${\tt TCGGGAGGGC\ ATAGCATCAA\ TAGATGTGCT\ GCCCCTCAGT\ CCGTTGATAC\ CTACTTGCTT\ TATCTGTCTA}$ 

3781 CGCTGAGATA GGTGCCTCAC TGATTAAGCA TTGGTAACTG TCAGACCAAG

GCGACTCTAT CCACGGAGTG ACTAATTCGT AACCATTGAC AGTCTGGTTC AAATGAGTAT ATATGAAATC

3851 ATTGATTTAA AACTTCATTT TTAATTTAAA AGGATCTAGG TGAAGATCCT TTTTGATAAT CTCATGACCA

TAACTAAATT TTGAAGTAAA AATTAAATTT TCCTAGATCC ACTTCTAGGA AAAACTATTA GAGTACTGGT

3921 AAATCCCTTA ACGTGAGTTT TCGTTCCACT GAGCGTCAGA CCCCGTAGAA AAGATCAAAG GATCTTCTTG

TTTAGGGAAT TGCACTCAAA AGCAAGGTGA CTCGCAGTCT GGGGCATCTT TTCTAGTTTC CTAGAAGAAC

3991 AGATCCTTTT TTTCTGCGCG TAATCTGCTG CTTGCAAACA AAAAAACCAC CGCTACCAGC GGTGGTTTGT

TCTAGGAAAA AAAGACGCGC ATTAGACGAC GAACGTTTGT TTTTTTGGTG GCGATGGTCG CCACCAAACA

4061 TTGCCGGATC AAGAGCTACC AACTCTTTTT CCGAAGGTAA CTGGCTTCAG CAGAGCGCAG ATACCAAATA

AACGGCCTAG TTCTCGATGG TTGAGAAAAA GGCTTCCATT GACCGAAGTC GTCTCGCGTC TATGGTTTAT

4131 CTGTCCTTCT AGTGTAGCCG TAGTTAGGCC ACCACTTCAA GAACTCTGTA GCACCGCCTA CATACCTCGC

GACAGGAAGA TCACATCGGC ATCAATCCGG TGGTGAAGTT CTTGAGACAT

4201 TCTGCTAATC CTGTTACCAG TGGCTGCTGC CAGTGGCGAT AAGTCGTGTC TTACCGGGTT GGACTCAAGA

AGACGATTAG GACAATGGTC ACCGACGACG GTCACCGCTA TTCAGCACAG AATGGCCCAA CCTGAGTTCT

4271 CGATAGTTAC CGGATAAGGC GCAGCGGTCG GGCTGAACGG GGGGTTCGTG CACACAGCCC AGCTTGGAGC

GCTATCAATG GCCTATTCCG CGTCGCCAGC CCGACTTGCC CCCCAAGCAC GTGTGTCGGG TCGAACCTCG

4341 GAACGACCTA CACCGAACTG AGATACCTAC AGCGTGAGCT ATGAGAAAGC GCCACGCTTC CCGAAGGGAG

CTTGCTGGAT GTGGCTTGAC TCTATGGATG TCGCACTCGA TACTCTTTCG

4411 AAAGGCGGAC AGGTATCCGG TAAGCGGCAG GGTCGGAACA GGAGAGCGCA CGAGGGAGCT TCCAGGGGGA

TTTCCGCCTG TCCATAGGCC ATTCGCCGTC CCAGCCTTGT CCTCTCGCGT

4481 AACGCCTGGT ATCTTTATAG TCCTGTCGGG TTTCGCCACC TCTGACTTGA GCGTCGATTT TTGTGATGCT

TTGCGGACCA TAGAAATATC AGGACAGCCC AAAGCGGTGG AGACTGAACT CGCAGCTAAA AACACTACGA

4551 CGTCAGGGGG GCGGAGCCTA TGGAAAAACG CCAGCAACGC GGCCTTTTTA CGGTTCCTGG CCTTTTGCTG

GCAGTCCCCC CGCCTCGGAT ACCTTTTTGC GGTCGTTGCG CCGGAAAAAT GCCAAGGACC GGAAAACGAC

Fig. 42 H

|            | GCCTTTTGCT                 |            | TTCCTGCGTT | ATCCCCTGAT | TCTGTGGATA |
|------------|----------------------------|------------|------------|------------|------------|
| ACCGTATTA( | CGCCTTTGAG<br>CGGAAAACGA   |            | AAGGACGCAA | TAGGGGACTA | AGACACCTAT |
| TGGCATAATO | G GCGGAAACTC               |            |            |            |            |
|            | TGAGCTGATA                 |            | CAGCCGAACG | ACCGAGCGCA | GCGAGTCAGT |
| GAGCGAGGAZ | A GCGGAAGAGC               |            | amagaammaa | macamaaaaa | CCCTCACTCA |
| CTCGCTCCT" | ACTCGACTAT<br>F CGCCTTCTCG |            | GTCGGCTTGC | 1990109091 | CGCICAGICA |
|            | GCCCAATACG                 |            | CTCCCCGCGC | GTTGGCCGAT | TCATTAATGC |
|            | G ACAGGTTTCC<br>CGGGTTATGC | GTTTGGCGGA | GAGGGGCGCG | CAACCGGCTA | AGTAATTACG |
| TCGACCGTG  | C TGTCCAAAGG               | τ          |            |            |            |
|            | CGACTGGAAA                 |            | AGCGCAACGC | AATTAATGTG | AGTTAGCTCA |
| •          |                            | CGCCCGTCAC | TCGCGTTGCG | TTAATTACAC | TCAATCGAGT |
| GAGTAATCC  | G TGGGGTCCGA               | 7          |            |            |            |
|            | TTACACTTTA                 |            | TCGTATGTTG | TGTGGAATTG | TGAGCGGATA |
| ACAATTTCA  | C ACAGGAAACA<br>AATGTGAAAT | ACGAAGGCCG | AGCATACAAC | ACACCTTAAC | ACTCGCCTAT |
| TGTTAAAGT  | G TGTCCTTTG1               | r          |            |            |            |
|            |                            |            |            |            |            |
| NcoI       |                            |            |            |            |            |
|            |                            |            | BssHII     |            |            |
| KpnI       |                            |            |            |            |            |
|            |                            |            | ~~~~~      |            |            |

4971 GCTATGACCA TGATTACGCC AAGCGCGCAA TTAACCCTCA CTAAAGGGAA CAAAAGCTGG GTAC
CGATACTGGT ACTAATGCGG TTCGCGCGTT AATTGGGAGT GATTTCCCTT

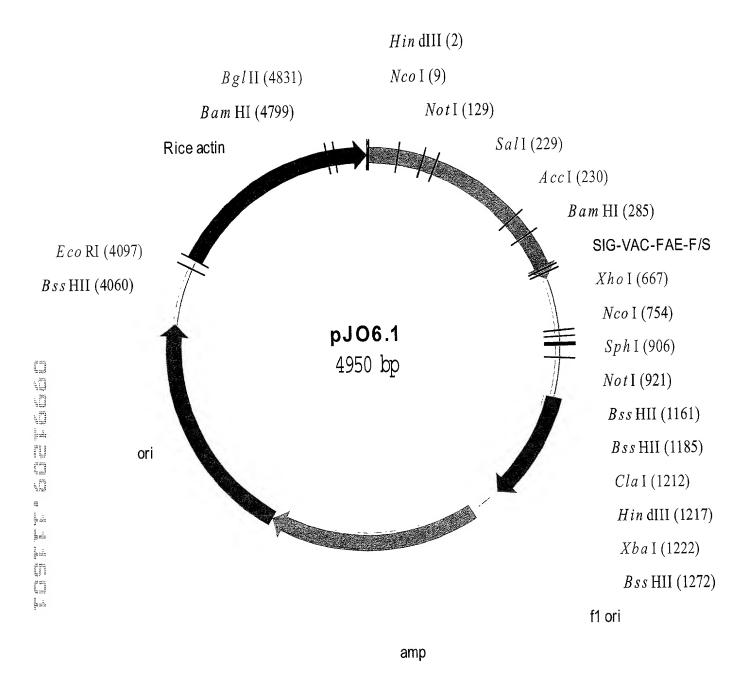


Fig. 43 A

### Sequence for pJO6

HindIII NcoI

 $_{\rm 1}$  AAGCTTACCA TGGCCCACGC CCGCGTCCTC CTCCTGGCGC TCGCCGTGCT GGCCACGGCC GCCGTCGCCG

TTCGAATGGT ACCGGGTGCG GGCGCAGGAG GAGGACCGCG AGCGGCACGA

NotI

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71 TCGCCTCCTC CTCCTCCTTC GCCGACTCCA ACCCGATCCG GCCCGTCACC GACCGCGCGC CCGCCTCCAC

AGCGGAGGAG GAGGAGGAAG CGGCTGAGGT TGGGCTAGGC CGGGCAGTGG

141 GCAGGGCATC TCCGAAGACC TCTACAGCCG TTTAGTCGAA ATGGCCACTA
TCTCCCAAGC TGCCTACGCC

CGTCCCGTAG AGGCTTCTGG AGATGTCGGC AAATCAGCTT TACCGGTGAT AGAGGGTTCG ACGGATGCGG

SalI

**7** -- -- T

AccI

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211 GACCTGTGCA ACATTCCGTC GACTATTATC AAGGGAGAGA AAATTTACAA
TTCTCAAACT GACATTAACG

CTGGACACGT TGTAAGGCAG CTGATAATAG TTCCCTCTCT TTTAAATGTT AAGAGTTTGA CTGTAATTGC

BamHI

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281 GATGGATCCT CCGCGACGAC AGCAGCAAAG AAATAATCAC CGTCTTCCGT GGCACTGGTA GTGATACGAA

CTACCTAGGA GGCGCTGCTG TCGTCGTTTC TTTATTAGTG GCAGAAGGCA CCGTGACCAT CACTATGCTT

351 TCTACAACTC GATACTAACT ACACCCTCAC GCCTTTCGAC ACCCTACCAC AATGCAACGG TTGTGAAGTA

 ${\tt AGATGTTGAG} \ \ {\tt CTATGATTGA} \ \ {\tt TGTGGGAGTG} \ \ {\tt CGGAAAGCTG} \ \ {\tt TGGGATGGTG}$   ${\tt TTACGTTGCC} \ \ {\tt AACACTTCAT}$ 

421 CACGGTGGAT ATTATATTGG ATGGGTCTCC GTCCAGGACC AAGTCGAGTC GCTTGTCAAA CAGCAGGTTA

GTGCCACCTA TAATATAACC TACCCAGAGG CAGGTCCTGG TTCAGCTCAG

491 GCCAGTATCC GGACTACGCG CTGACCGTGA CCGGCCACKC CCTCGGCGCC TCCCTGGCGG CACTCACTGC

Fig. 43 B

561 CGCCCAGCTG TCTGCGACAT ACGACAACAT CCGCCTGTAC ACCTTCGGCG

AACCGCGCAG CGGCAATCAG

GCGCGTCGAC AGACGCTGTA TGCTGTTGTA GGCGGACATG TGGAAGCCGC

GCGGGTCGAC AGACGCTGTA TGCTGTTGTA GGCGGACATG TGGAAGCCGC TTGGCGCGTC GCCGTTAGTC

### XhoI

631 GCCTTCGCGT CGTACATGAA CGATGCCTTC CAAGCCTCGA GCCCAGATAC GACGCAGTAT TTCCGGGTCA

CGGAAGCGCA GCATGTACTT GCTACGGAAG GTTCGGAGCT CGGGTCTATG

NcoI

701 CTCATGCCAA CGACGGCATC CCAAACCTGC CCCCGGTGGA GCAGGGGTAC GCCCATGGCG GTGTAGAGTA

GAGTACGGTT GCTGCCGTAG GGTTTGGACG GGGGCCACCT CGTCCCCATG

771 CTGGAGCGTT GATCCTTACA GCGCCCAGAA CACATTTGTC TGCACTGGGG ATGAAGTGCA GTGCTGTGAG

GACCTCGCAA CTAGGAATGT CGCGGGTCTT GTGTAAACAG ACGTGACCCC TACTTCACGT CACGACACTC

SphI

841 GCCCAGGGCG GACAGGGTGT GAATAATGCG CACACGACTT ATTTTGGGAT GACGAGCGGC GCATGCACCT

CGGGTCCCGC CTGTCCCACA CTTATTACGC GTGTGCTGAA TAAAACCCTA

# NotI

911 GGCCGGTCGC GGCCGCGGAA ACCACTGAAG GATGAGCTGT AAAGAAGCAG ATCGTTCAAA CATTTGGCAA

CCGGCCAGCG CCGGCGCCTT TGGTGACTTC CTACTCGACA TTTCTTCGTC TAGCAAGTTT GTAAACCGTT

981 TAAAGTTTCT TAAGATTGAA TCCTGTTGCC GGTCTTGCGA TGATTATCAT ATAATTTCTG TTGAATTACG

ATTTCAAAGA ATTCTAACTT AGGACAACGG CCAGAACGCT ACTAATAGTA TATTAAAGAC AACTTAATGC

1051 TTAAGCATGT AATAATTAAC ATGTAATGCA TGACGTTATT TATGAGATGG GTTTTTATGA TTAGAGTCCC

AATTCGTACA TTATTAATTG TACATTACGT ACTGCAATAA ATACTCTACC CAAAAATACT AATCTCAGGG

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1121 GCAATTATAC ATTTAATACG CGATAGAAAA CAAAATATAG CGCGCAAACT AGGATAAATT ATCGCGCGCG

#### XbaI

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## ClaI HindIII

1191 GTGTCATCTA TGTTACTAGA TCGATAAGCT TCTAGAGCGG CCGGTGGAGC TCCAATTCGC CCTATAGTGA

CACAGTAGAT ACAATGATCT AGCTATTCGA AGATCTCGCC GGCCACCTCG AGGTTAAGCG GGATATCACT

### BssHII

CAGCATAATG CGCGCGAGTG ACCGGCAGCA AAATGTTGCA GCACTGACCC

- 1331 CTTAATCGCC TTGCAGCACA TCCCCCTTTC GCCAGCTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC
- GAATTAGCGG AACGTCGTGT AGGGGGAAAG CGGTCGACCG CATTATCGCT
- 1401 CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGGACGC GCCCTGTAGC GGCGCATTAA GCGCGGCGGG
- GAAGGGTTGT CAACGCGTCG GACTTACCGC TTACCCTGCG CGGGACATCG
- 1471 TGTGGTGGTT ACGCGCAGCG TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT CGCTTCTTC
- ACACCACCAA TGCGCGTCGC ACTGGCGATG TGAACGGTCG CGGGATCGCG
- 1541 CCTTCCTTTC TCGCCACGTT CGCCGGCTTT CCCCGTCAAG CTCTAAATCG GGGGCTCCCT TTAGGGTTCC
- GGAAGGAAAG AGCGGTGCAA GCGGCCGAAA GGGGCAGTTC GAGATTTAGC
- 1611 GATTTAGTGC TTTACGGCAC CTCGACCCCA AAAAACTTGA TTAGGGTGAT GGTTCACGTA GTGGGCCATC
- CTAAATCACG AAATGCCGTG GAGCTGGGGT TTTTTGAACT AATCCCACTA
- 1681 GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA ATAGTGGACT CTTGTTCCAA
- CGGGACTATC TGCCAAAAAG CGGGAAACTG CAACCTCAGG TGCAAGAAAT TATCACCTGA GAACAAGGTT

1751 ACTGGAACAA CACTCAACCC TATCTCGGTC TATTCTTTTG ATTTATAAGG GATTTTGCCG ATTTCGGCCT

TGACCTTGTT GTGAGTTGGG ATAGAGCCAG ATAAGAAAC TAAATATTCC CTAAAACGGC TAAAGCCGGA

1821 ATTGGTTAAA AAATGAGCTG ATTTAACAAA AATTTAACGC GAATTTTAAC AAAATATTAA CGCTTACAAT

TAACCAATTT TTTACTCGAC TAAATTGTTT TTAAATTGCG CTTAAAATTG

1891 TTAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA

AATCCACCGT GAAAAGCCCC TTTACACGCG CCTTGGGGAT AAACAAATAA AAAGATTTAT GTAAGTTTAT

1961 TGTATCCGCT CATGAGACAA TAACCCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT

ACATAGGCGA GTACTCTGTT ATTGGGACTA TTTACGAAGT TATTATAACT

2031 TCAACATTTC CGTGTCGCCC TTATTCCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC TCACCCAGAA

AGTTGTAAAG GCACAGCGGG AATAAGGGAA AAAACGCCGT AAAACGGAAGGACAAAAACG AGTGGGTCTT

2101 ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG CACGAGTGGG TTACATCGAA CTGGATCTCA

TGCGACCACT TTCATTTTCT ACGACTTCTA GTCAACCCAC GTGCTCACCC AATGTAGCTT GACCTAGAGT

2171 ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT TTAAAGTTCT

2241 GCTATGTGGC GCGGTATTAT CCCGTATTGA CGCCGGGCAA GAGCAACTCG

CGATACACCG CGCCATAATA GGGCATAACT GCGGCCCGTT CTCGTTGAGCCCAGCGGCGTA TGTGATAAGA

2311 CAGAATGACT TGGTTGAGTA CTCACCAGTC ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT

GTCTTACTGA ACCAACTCAT GAGTGGTCAG TGTCTTTTCG TAGAATGCCT ACCGTACTGT CATTCTCTTA

2381 TATGCAGTGC TGCCATAACC ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA TCGGAGGACC

ATACGTCACG ACGGTATTGG TACTCACTAT TGTGACGCCG GTTGAATGAA

2451 GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT GTAACTCGCC TTGATCGTTG GGAACCGGAG CTTCCTCGAT TGGCGAAAAA ACGTGTTGTA CCCCCTAGTA CATTGAGCGG AACTAGCAAC CCTTGGCCTC

2521 CTGAATGAAG CCATACCAAA CGACGAGCGT GACACCACGA TGCCTGTAGC AATGGCAACA ACGTTGCGCA

GACTTACTTC GGTATGGTTT GCTGCTCGCA CTGTGGTGCT ACGGACATCG
TTACCGTTGT TGCAACGCGT

2591 AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA ACAATTAATA GACTGGATGG AGGCGGATAA

TTGATAATTG ACCGCTTGAT GAATGAGATC GAAGGGCCGT TGTTAATTAT

2661 AGTTGCAGGA CCACTTCTGC GCTCGGCCCT TCCGGCTGGC TGGTTTATTG

TCAACGTCCT GGTGAAGACG CGAGCCGGGA AGGCCGACCG ACCAAATAAC GACTATTTAG ACCTCGGCCA

2731 GAGCGTGGGT CTCGCGGTAT CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC GTAGTTATCT

CTCGCACCCA GAGCGCCATA GTAACGTCGT GACCCCGGTC TACCATTCGG GAGGGCATAG CATCAATAGA

2801 ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG ACAGATCGCT GAGATAGGTG CCTCACTGAT

TGTGCTGCCC CTCAGTCCGT TGATACCTAC TTGCTTTATC TGTCTAGCGA CTCTATCCAC GGAGTGACTA

2871 TAAGCATTGG TAACTGTCAG ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTTAA

ATTCGTAACC ATTGACAGTC TGGTTCAAAT GAGTATATAT GAAATCTAAC TAAATTTTGA AGTAAAAATT

2941 TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT CCCTTAACGT GAGTTTTCGT

AAATTTTCCT AGATCCACTT CTAGGAAAAA CTATTAGAGT ACTGGTTTTA

3011 TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC TTCTTGAGAT

AGGTGACTCG CAGTCTGGGG CATCTTTTCT AGTTTCCTAG AAGAACTCTA

3081 CTGCTGCTTG CAAACAAAA AACCACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA GCTACCAACT

GACGACGAAC GTTTGTTTTT TTGGTGGCGA TGGTCGCCAC CAAACAAACG GCCTAGTTCT CGATGGTTGA

3151 CTTTTCCGA AGGTAACTGG CTTCAGCAGA GCGCAGATAC CAAATACTGT CCTTCTAGTG TAGCCGTAGT

GAAAAAGGCT TCCATTGACC GAAGTCGTCT CGCGTCTATG GTTTATGACA GGAAGATCAC ATCGGCATCA

- 3291 TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT AGTTACCGGA TAAGGCGCAG ACGACGGTCA CCGCTATTCA GCACAGAATG GCCCAACCTG AGTTCTGCTA

TCAATGGCCT ATTCCGCGTC

- 3361 CGGTCGGGCT GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC
  GACCTACACC GAACTGAGAT
- 3431 ACCTACAGCG TGAGCTATGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT ATCCGGTAAG
- TGGATGTCGC ACTCGATACT CTTTCGCGGT GCGAAGGGCT TCCCTCTTTC
- $3\,5\,0\,1$  CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA GGGGGAAACG CCTGGTATCT TTATAGTCCT
- GCCGTCCCAG CCTTGTCCTC TCGCGTGCTC CCTCGAAGGT CCCCCTTTGC GGACCATAGA AATATCAGGA
- 3571 GTCGGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTTGT GATGCTCGTC
  AGGGGGGCGG AGCCTATGGA

CAGCCCAAAG CGGTGGAGAC TGAACTCGCA GCTAAAAACA CTACGAGCAG TCCCCCCGCC TCGGATACCT

- 3641 AAAACGCCAG CAACGCGGCC TTTTTACGGT TCCTGGCCTT TTGCTGGCCT
- TTTTGCGGTC GTTGCGCCGG AAAAATGCCA AGGACCGGAA AACGACCGGA AAACGAGTGT ACAAGAAAGG
- 3711 TGCGTTATCC CCTGATTCTG TGGATAACCG TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGCAGC
- ACGCAATAGG GGACTAAGAC ACCTATTGGC ATAATGGCGG AAACTCACTC GACTATGGCG AGCGGCGTCG
- 3781 CGAACGACCG AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAAA CCGCCTCTCC
- GCTTGCTGGC TCGCGTCGCT CAGTCACTCG CTCCTTCGCC TTCTCGCGGG
  TTATGCGTTT GGCGGAGAGG
- 3851 CCGCGCGTTG GCCGATTCAT TAATGCAGCT GGCACGACAG GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG
- GGCGCGCAAC CGGCTAAGTA ATTACGTCGA CCGTGCTGTC CAAAGGGCTG ACCTTTCGCC CGTCACTCGC
- 3921 CAACGCAATT AATGTGAGTT AGCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT
- GTTGCGTTAA TTACACTCAA TCGAGTGAGT AATCCGTGGG GTCCGAAATG

3991 ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA TGACCATGAT TACGCCAAGC

TACAACACAC CTTAACACTC GCCTATTGTT AAAGTGTGTC CTTTGTCGAT ACTGGTACTA ATGCGGTTCG

BSSHII ECORI

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4061 GCGCAATTAA CCCTCACTAA AGGGAACAAA AGCTGGAATT CCACAATGAA CAATAATAAG ATTAAAATAG

CGCGTTAATT GGGAGTGATT TCCCTTGTTT TCGACCTTAA GGTGTTACTT GTTATTATTC TAATTTTATC

4131 CTTGCCCCCG TTGCAGCGAT GGGTATTTTT TCTAGTAAAA TAAAAGATAA ACTTAGACTC AAAACATTTA

GAACGGGGGC AACGTCGCTA CCCATAAAAA AGATCATTTT ATTTTCTATT

4201 CAAAAACAAC CCCTAAAGTC CTAAAGCCCA AAGTGCTATG CACGATCCAT AGCAAGCCCA GCCCAACCCA

GTTTTGTTG GGGATTTCAG GATTTCGGGT TTCACGATAC GTGCTAGGTA

4271 ACCCAACCCA ACCCACCCCA GTGCAGCCAA CTGGCAAATA GTCTCCACCC CCGGCACTAT CACCGTGAGT

 ${\tt TGGGTTGGGT\ TGGGTGGGGT\ CACGTCGGTT\ GACCGTTTAT\ CAGAGGTGGG\ GGCCGTGATA\ GTGGCACTCA}$ 

4341 TGTCCGCACC ACCGCACGTC TCGCAGCCAA AAAAAAAAA AGAAAGAAAA AAAAGAAAAA GAAAAACAGC

4411 AGGTGGGTCC GGGTCGTGGG GGCCGGAAAA GCGAGGAGGA TCGCGAGCAG

TCCACCCAGG CCCAGCACCC CCGGCCTTTT CGCTCCTCCT AGCGCTCGTC GCTGCTCCGG GCCGGGAGGG

4481 TCCGCTTCCA AAGAAACGCC CCCCATCGCC ACTATATACA TACCCCCCCC TCTCCTCCCA TCCCCCCAAC

AGGCGAAGGT TTCTTTGCGG GGGGTAGCGG TGATATATGT ATGGGGGGGGG AGAGGAGGGT AGGGGGGTTG

4551 CCTACCACCA CCACCACCAC CACCTCCTCC CCCCTCGCTG CCGGACGACG

 ${\tt GGATGGTGGT} \ \ {\tt GTGGAGGAGG} \ \ {\tt GGGGAGCGAC} \ \ {\tt GGCCTGCTGC} \\ \ \ {\tt TCGAGGAGGG} \ \ {\tt GGGAGGGGGA} \\$ 

4621 CCGCCGCCGC CGGTAACCAC CCCGCCCCTC TCCTCTTTCT TTCTCCGTTT

Fig 43H

GGCGGCGGCG GCCATTGGTG GGGCGGGGAG AGGAGAAAGA AAGAGGCAAA AAAAAAAGCA GAGCCAGAGC

4691 ATCTTTGGCC TTGGTAGTTT GGGTGGGCGA GAGCGGCTTC GTCGCCCAGA TCGGTGCGCG GGAGGGGCGG

TAGAAACCGG AACCATCAAA CCCACCCGCT CTCGCCGAAG CAGCGGGTCT AGCCACGCGC CCTCCCCGGC

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4761 GATCTCGCGG CTGGCGTCTC CGGGCGTGAG TCGGCCCGGA TCCTCGCGGG

GAATGGGGCT CTCGGATGTA

CTAGAGCGCC GACCGCAGAG GCCCGCACTC AGCCGGGCCT AGGAGCGCCC
CTTACCCCGA GAGCCTACAT

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4831 GATCTTCTTT CTTTCTTCTT TTTGTGGTAG AATTTGAATC CCTCAGCATT GTTCATCGGT AGTTTTTCTT

CTAGAAGAAA GAAAGAAGAA AAACACCATC TTAAACTTAG GGAGTCGTAA CAAGTAGCCA TCAAAAAGAA

4901 TTCATGATTT GTGACAAATG CAGCCTCGTG CGGAGCTTTT TTGTAGGTAG
AAGTACTAAA CACTGTTTAC GTCGGAGCAC GCCTCGAAAA AACATCCATC

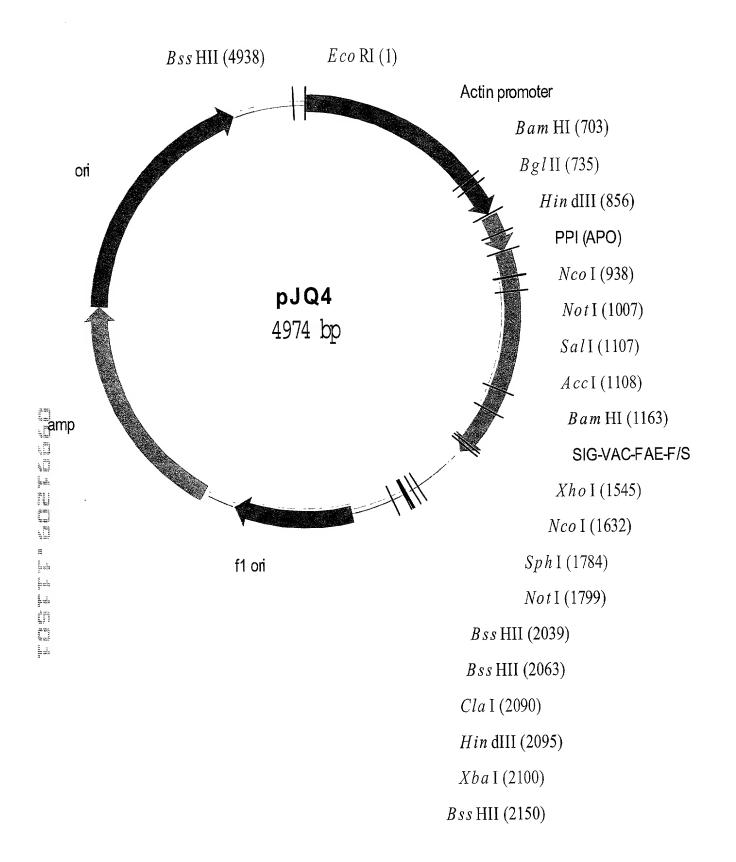


Fig. 44 A

### Sequence for pJQ4

EcoRI

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1 AATTCCACAA TGAACAATAA TAAGATTAAA ATAGCTTGCC CCCGTTGCAG CGATGGGTAT TTTTTCTAGT

TTAAGGTGTT ACTTGTTATT ATTCTAATTT TATCGAACGG GGGCAACGTC

71 AAAATAAAAG ATAAACTTAG ACTCAAAACA TTTACAAAAA CAACCCCTAA AGTCCTAAAG CCCAAAGTGC

TTTTATTTC TATTTGAATC TGAGTTTTGT AAATGTTTTT GTTGGGGATT TCAGGATTTC GGGTTTCACG

211 AATAGTCTCC ACCCCCGGCA CTATCACCGT GAGTTGTCCG CACCACCGCA

TTATCAGAGG TGGGGGCCGT GATAGTGGCA CTCAACAGGC GTGGTGGCGT GCAGAGCGTC GGTTTTTTTT

281 AAAAAGAAAG AAAAAAAAAA CAGCAGGTGG GTCCGGGTCG

351 AGGATCGCGA GCAGCGACGA GGCCCGGCCC TCCCTCCGCT TCCAAAGAAA CGCCCCCCAT CGCCACTATA

TCCTAGCGCT CGTCGCTGCT CCGGGCCGGG AGGGAGGCGA AGGTTTCTTT GCGGGGGGTA GCGGTGATAT

421 TACATACCCC CCCCTCTCCT CCCATCCCCC CAACCCTACC ACCACCACCA CCACCACCTC CTCCCCCCTC.

ATGTATGGGG GGGGAGAGGA GGGTAGGGGG GTTGGGATGG TGGTGGTGGT

491 GCTGCCGGAC GACGAGCTCC TCCCCCCTCC CCCTCCGCCG CCGCCGGTAA

CGACGGCCTG CTGCTCGAGG AGGGGGGAGG GGGAGGCGGC GGCGGCCATT

561 TTCTTTCTCC GTTTTTTTT TCGTCTCGGT CTCGATCTTT GGCCTTGGTA GTTTGGGTGG GCGAGAGCGG

AAGAAAGAG CAAAAAAAA AGCAGAGCCA GAGCTAGAAA CCGGAACCAT

631 CTTCGTCGCC CAGATCGGTG CGCGGGAGGG GCGGGATCTC GCGGCTGGCG

Fig. 44B

GAAGCAGCGG GTCTAGCCAC GCGCCCTCCC CGCCCTAGAG CGCCGACCGC AGAGGCCCGC ACTCAGCCGG

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701 CGGATCCTCG CGGGGAATGG GGCTCTCGGA TGTAGATCTT CTTTCTTTCT TCTTTTTGTG GTAGAATTTG

GCCTAGGAGC GCCCCTTACC CCGAGAGCCT ACATCTAGAA GAAAGAAAGA AGAAAAACAC CATCTTAAAC

771 AATCCCTCAG CATTGTTCAT CGGTAGTTTT TCTTTTCATG ATTTGTGACA AATGCAGCCT CGTGCGGAGC

TTAGGGAGTC GTAACAAGTA GCCATCAAAA AGAAAAGTAC TAAACACTGT TTACGTCGGA GCACGCCTCG

### HindIII

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841 TTTTTTGTAG GTAGAAGCTT ACMATGGMCG TGCACAAGGA GGTSAACTTC GTSGCCTACC TCCTGATCGT

AAAAAACATC CATCTTCGAA TGKTACCKGC ACGTGTTCCT CCASTTGAAG CASCGGATGG AGGACTAGCA

# NcoI

911 SCTCGGCCTC CTCTTGCTCG TSTCCGCCAT GGAGCACGTG GACGCCAAGG CCTGCACCCK CGAGTGCGGC

SGAGCCGGAG GAGAACGAGC ASAGGCGGTA CCTCGTGCAC CTGCGGTTCC GGACGTGGGM GCTCACGCCG

## NotI

981 AACCTCGGCT TCGGCATCTG CCCGGCGGCC GCCTCCACGC AGGGCATCTC

CGAAGACCTC TACAGCCGTT

TTGGAGCCGA AGCCGTAGAC GGGCCGCCGG CGGAGGTGCG TCCCGTAGAG GCTTCTGGAG ATGTCGGCAA

SalI

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AccI

1051 TAGTCGAAAT GGCCACTATC TCCCAAGCTG CCTACGCCGA CCTGTGCAAC ATTCCGTCGA CTATTATCAA

ATCAGCTTTA CCGGTGATAG AGGGTTCGAC GGATGCGGCT GGACACGTTG TAAGGCAGCT GATAATAGTT

BamHI

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1121 GGGAGAAAA ATTTACAATT CTCAAACTGA CATTAACGGA TGGATCCTCC GCGACGACAG CAGCAAAGAA

Fig. 44 C

CCCTCTCTT TAAATGTTAA GAGTTTGACT GTAATTGCCT ACCTAGGAGG

1191 ATAATCACCG TCTTCCGTGG CACTGGTAGT GATACGAATC TACAACTCGA
TACTAACTAC ACCCTCACGC

TATTAGTGGC AGAAGGCACC GTGACCATCA CTATGCTTAG ATGTTGAGCT ATGATTGATG TGGGAGTGCG

1261 CTTTCGACAC CCTACCACAA TGCAACGGTT GTGAAGTACA CGGTGGATAT
TATATTGGAT GGGTCTCCGT

GAAAGCTGTG GGATGGTGTT ACGTTGCCAA CACTTCATGT GCCACCTATA ATATAACCTA CCCAGAGGCA

1331 CCAGGACCAA GTCGAGTCGC TTGTCAAACA GCAGGTTAGC CAGTATCCGG ACTACGCGCT GACCGTGACC

 ${\tt GGTCCTGGTT\ CAGCTCAGCG\ AACAGTTTGT\ CGTCCAATCG\ GTCATAGGCC\ TGATGCGCGA\ CTGGCACTGG}$ 

1401 GGCCACKCCC TCGGCGCCTC CCTGGCGGCA CTCACTGCCG CCCAGCTGTC TGCGACATAC GACAACATCC

1471 GCCTGTACAC CTTCGGCGAA CCGCGCAGCG GCAATCAGGC CTTCGCGTCG
TACATGAACG ATGCCTTCCA

CGGACATGTG GAAGCCGCTT GGCGCGTCGC CGTTAGTCCG GAAGCGCAGC ATGTACTTGC TACGGAAGGT

### XhoI

1541 AGCCTCGAGC CCAGATACGA CGCAGTATTT CCGGGTCACT CATGCCAACG ACGGCATCCC AAACCTGCCC

TCGGAGCTCG GGTCTATGCT GCGTCATAAA GGCCCAGTGA GTACGGTTGC
TGCCGTAGGG TTTGGACGGG

#### NcoI

1611 CCGGTGGAGC AGGGGTACGC CCATGGCGGT GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA

1681 CATTTGTCTG CACTGGGGAT GAAGTGCAGT GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA

GTAAACAGAC GTGACCCCTA CTTCACGTCA CGACACTCCG GGTCCCGCCT GTCCCACACT TATTACGCGT

SphI

NotI

1751 CACGACTTAT TTTGGGATGA CGAGCGGCGC ATGCACCTGG CCGGTCGCGG CCGCGGAAAC CACTGAAGGA

GTGCTGAATA AAACCCTACT GCTCGCCGCG TACGTGGACC GGCCAGCGCC GGCGCCTTTG GTGACTTCCT

182	21 TGAGCTGTAA	AGAAGCAGAT	CGTTCAAACA	TTTGGCAATA	AAGTTTCTTA
AGATTGAATC CTGTTGCCGG					
	ACTCGACATT	TCTTCGTCTA	GCAAGTTTGT	AAACCGTTAT	TTCAAAGAAT
TCTAACTTAG GACAACGGCC					

1891 TCTTGCGATG ATTATCATAT AATTTCTGTT GAATTACGTT AAGCATGTAA
TAATTAACAT GTAATGCATG

AGAACGCTAC TAATAGTATA TTAAAGACAA CTTAATGCAA TTCGTACATT
ATTAATTGTA CATTACGTAC

1961 ACGTTATTTA TGAGATGGGT TTTTATGATT AGAGTCCCGC AATTATACAT TTAATACGCG ATAGAAAACA

TGCAATAAAT ACTCTACCCA AAAATACTAA TCTCAGGGCG TTAATATGTA AATTATGCGC TATCTTTTGT

XbaI

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2031 AAATATAGCG CGCAAACTAG GATAAATTAT CGCGCGCGGT GTCATCTATG

XbaI BssHII

2101 TAGAGCGGCC GGTGGAGCTC CAATTCGCCC TATAGTGAGT CGTATTACGC GCGCTCACTG GCCGTCGTTT

ATCTCGCCGG CCACCTCGAG GTTAAGCGGG ATATCACTCA GCATAATGCG

2171 TACAACGTCG TGACTGGGAA AACCCTGGCG TTACCCAACT TAATCGCCTT GCAGCACATC CCCCTTTCGC

ATGTTGCAGC ACTGACCCTT TTGGGACCGC AATGGGTTGA ATTAGCGGAA

2241 CAGCTGGCGT AATAGCGAAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT TGCGCAGCCT GAATGGCGAA

GTCGACCGCA TTATCGCTTC TCCGGGCGTG GCTAGCGGGA AGGGTTGTCA ACGCGTCGGA CTTACCGCTT

2311 TGGGACGCGC CCTGTAGCGG CGCATTAAGC GCGGCGGGTG TGGTGGTTAC GCGCAGCGTG ACCGCTACAC

ACCCTGCGCG GGACATCGCC GCGTAATTCG CGCCGCCCAC ACCACCAATG

 $23\,81$  TTGCCAGCGC CCTAGCGCCC GCTCCTTTCG CTTTCTTCCC TTCCTTTCTC GCCACGTTCG CCGGCTTTCC

AACGGTCGCG GGATCGCGGG CGAGGAAAGC GAAAGAAGGG AAGGAAAGAG CGGTGCAAGC GGCCGAAAGG 2451 CCGTCAAGCT CTAAATCGGG GGCTCCCTTT AGGGTTCCGA TTTAGTGCTT TACGGCACCT CGACCCCAAA

GGCAGTTCGA GATTTAGCCC CCGAGGGAAA TCCCAAGGCT AAATCACGAA ATGCCGTGGA GCTGGGGTTT

2521 AAACTTGATT AGGGTGATGG TTCACGTAGT GGGCCATCGC CCTGATAGAC GGTTTTTCGC CCTTTGACGT

TTTGAACTAA TCCCACTACC AAGTGCATCA CCCGGTAGCG GGACTATCTG

2591 TGGAGTCCAC GTTCTTTAAT AGTGGACTCT TGTTCCAAAC TGGAACAACA CTCAACCCTA TCTCGGTCTA

ACCTCAGGTG CAAGAATTA TCACCTGAGA ACAAGGTTTG ACCTTGTTGT GAGTTGGGAT AGAGCCAGAT

2661 TTCTTTTGAT TTATAAGGGA TTTTGCCGAT TTCGGCCTAT TGGTTAAAAA ATGAGCTGAT TTAACAAAAA

AAGAAAACTA AATATTCCCT AAAACGGCTA AAGCCGGATA ACCAATTTTT TACTCGACTA AATTGTTTTT

2731 TTTAACGCGA ATTTTAACAA AATATTAACG CTTACAATTT AGGTGGCACT TTTCGGGGAA ATGTGCGCGG

AAATTGCGCT TAAAATTGTT TTATAATTGC GAATGTTAAA TCCACCGTGA AAAGCCCCTT TACACGCGCC

2801 AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA

TTGGGGATAA ACAAATAAAA AGATTTATGT AAGTTTATAC ATAGGCGAGT ACTCTGTTAT TGGGACTATT

2871 ATGCTTCAAT AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG
TGTCGCCCTT ATTCCCTTTT

TACGAAGTTA TTATAACTTT TTCCTTCTCA TACTCATAAG TTGTAAAGGC ACAGCGGGAA TAAGGGAAAA

2941 TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA

AACGCCGTAA AACGGAAGGA CAAAAACGAG TGGGTCTTTG CGACCACTTT CATTTTCTAC GACTTCTAGT

3011 GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC

CAACCCACGT GCTCACCCAA TGTAGCTTGA CCTAGAGTTG TCGCCATTCT AGGAACTCTC AAAAGCGGGG

3081 GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTATTGACG

CTTCTTGCAA AAGGTTACTA CTCGTGAAAA TTTCAAGACG ATACACCGCG CCATAATAGG GCATAACTGC

3151 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG

GGCCCGTTCT CGTTGAGCCA GCGGCGTATG TGATAAGAGT CTTACTGAAC CAACTCATGA GTGGTCAGTG

3221 AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC

TCTTTTCGTA GAATGCCTAC CGTACTGTCA TTCTCTTAAT ACGTCACGAC GGTATTGGTA CTCACTATTG

3291 ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG

TGACGCCGGT TGAATGAAGA CTGTTGCTAG CCTCCTGGCT TCCTCGATTG GCGAAAAAAC GTGTTGTACC

3361 GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA

CCCTAGTACA TTGAGCGGAA CTAGCAACCC TTGGCCTCGA CTTACTTCGG TATGGTTTGC TGCTCGCACT

3431 CACCACGATG CCTGTAGCAA TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT

GTGGTGCTAC GGACATCGTT ACCGTTGTTG CAACGCGTTT GATAATTGAC CGCTTGATGA ATGAGATCGA

3501 TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC

AGGGCCGTTG TTAATTATCT GACCTACCTC CGCCTATTTC AACGTCCTGG TGAAGACGCG AGCCGGGAAG

3571 CGGCTGGCTG GTTTATTGCT GATAAATCTG GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT

GCCGACCGAC CAAATAACGA CTATTTAGAC CTCGGCCACT CGCACCCAGA GCGCCATAGT AACGTCGTGA

3641 GGGGCCAGAT GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA

CCCCGGTCTA CCATTCGGGA GGGCATAGCA TCAATAGATG TGCTGCCCCT CAGTCCGTTG ATACCTACTT

3711 CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT

3781 CATATACT TTAGATTGAT TTAAAACTTC ATTTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA

GTATATATGA AATCTAACTA AATTTTGAAG TAAAAATTAA ATTTTCCTAG ATCCACTTCT AGGAAAAACT

3851 TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT CAGACCCCGT AGAAAAGATC

ATTAGAGTAC TGGTTTTAGG GAATTGCACT CAAAAGCAAG GTGACTCGCA GTCTGGGGCA TCTTTTCTAG 3921 AAAGGATCTT CTTGAGATCC TTTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC

TTTCCTAGAA GAACTCTAGG AAAAAAAGAC GCGCATTAGA CGACGAACGT TTGTTTTTTT GGTGGCGATG

3991 CAGCGGTGGT TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAGGTAACTGGCT TCAGCAGAGC

GTCGCCACCA AACAAACGGC CTAGTTCTCG ATGGTTGAGA AAAAGGCTTC CATTGACCGA AGTCGTCTCG

4061 GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG

CGTCTATGGT TTATGACAGG AAGATCACAT CGGCATCAAT CCGGTGGTGA AGTTCTTGAG ACATCGTGGC

4131 CCTACATACC TCGCTCTGCT AATCCTGTTA CCAGTGGCTG CTGCCAGTGG

. GGATGTATGG AGCGAGACGA TTAGGACAAT GGTCACCGAC GACGGTCACC GCTATTCAGC ACAGAATGGC

4201 GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT CGTGCACACA

CCAACCTGAG TTCTGCTATC AATGGCCTAT TCCGCGTCGC CAGCCCGACT TGCCCCCCAA GCACGTGTGT

 $4\,2\,7\,1$  GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG

4341 CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGG CGCACGAGGG

GAAGGGCTTC CCTCTTTCCG CCTGTCCATA GGCCATTCGC CGTCCCAGCC TTGTCCTCTC GCGTGCTCCC

4411 AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG

TCGAAGGTCC CCCTTTGCGG ACCATAGAAA TATCAGGACA GCCCAAAGCG GTGGAGACTG AACTCGCAGC

4481 ATTTTTGTGA TGCTCGTCAG GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC

TAAAAACACT ACGAGCAGTC CCCCCGCCTC GGATACCTTT TTGCGGTCGT TGCGCCGGAA AAATGCCAAG

4551 CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA

GACCGGAAAA CGACCGGAAA ACGAGTGTAC AAGAAAGGAC GCAATAGGGG ACTAAGACAC CTATTGGCAT

4621 TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAGCGAGCGAGT CAGTGAGCGA

AATGGCGGAA ACTCACTCGA CTATGGCGAG CGGCGTCGGC TTGCTGGCTCGCTCACTCACTCGCT

4691 GGAAGCGGAA GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC CGATTCATTA ATGCAGCTGG

CCTTCGCCTT CTCGCGGGTT ATGCGTTTGG CGGAGAGGGG CGCGCAACCG GCTAAGTAAT TACGTCGACC

4761 CACGACAGGT TTCCCGACTG GAAAGCGGGC AGTGAGCGCA ACGCAATTAA TGTGAGTTAG CTCACTCATT

4831 AGGCACCCCA GGCTTTACAC TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT

TCCGTGGGT CCGAAATGTG AAATACGAAG GCCGAGCATA CAACACCCT TAACACTCGC CTATTGTTAA

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4901 TCACACAGGA AACAGCTATG ACCATGATTA CGCCAAGCGC GCAATTAACC CTCACTAAAG GGAACAAAAG

 ${\tt AGTGTGTCCT\ TTGTCGATAC\ TGGTACTAAT\ GCGGTTCGCG\ CGTTAATTGG}\\ {\tt GAGTGATTTC\ CCTTGTTTTC\ }$ 

EcoR

4971 CTGG GACC

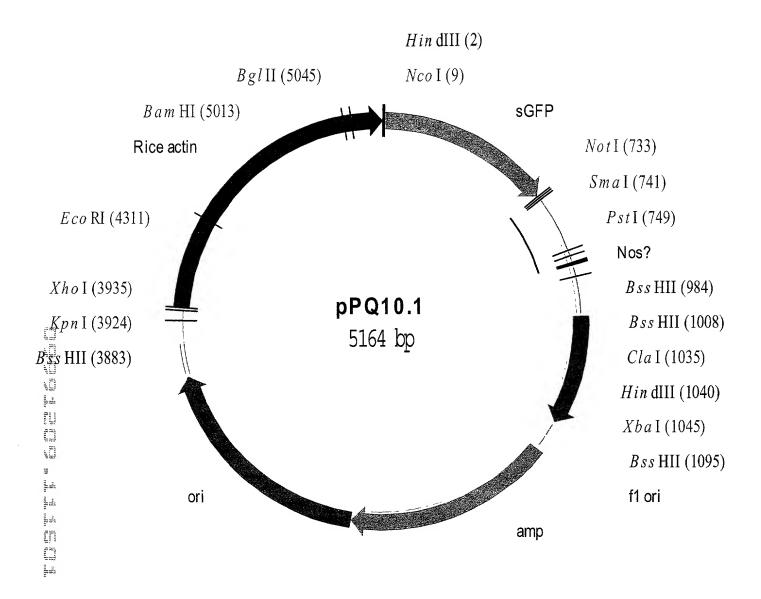


Fig. 45 A

### Sequence for pPQ10.1

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- 1 AAGCTTACCA TGGTGAGCAA GGGCGAGGAG CTGTTCACCG GGGTGGTGCC CATCCTGGTC GAGCTGGACG
- TTCGAATGGT ACCACTCGTT CCCGCTCCTC GACAAGTGGC CCCACCACGG
- 71 GCGACGTGAA CGGCCACAAG TTCAGCGTGT CCGGCGAGGG CGAGGGCGAT GCCACCTACG GCAAGCTGAC
- CGCTGCACTT GCCGGTGTTC AAGTCGCACA GGCCGCTCCC GCTCCCGCTA
- 141 CCTGAAGTTC ATCTGCACCA CCGGCAAGCT GCCCGTGCCC TGGCCCACCC TCGTGACCAC CTTCACCTAC
- ${\tt GGACTTCAAG} \ \ {\tt TAGACGTGGT} \ \ {\tt GGCCGTTCGA} \ \ {\tt CGGGCACGGG} \ \ {\tt ACCGGGTGGG} \\ {\tt AGCACTGGTG} \ \ {\tt GAAGTGGATG} \\$
- 211 GGCGTGCAGT GCTTCAGCCG CTACCCCGAC CACATGAAGC AGCACGACTT CTTCAAGTCC GCCATGCCCG
- CCGCACGTCA CGAAGTCGGC GATGGGGCTG GTGTACTTCG TCGTGCTGAA GAAGTTCAGG CGGTACGGGC
- 281 AAGGCTACGT CCAGGAGCGC ACCATCTTCT TCAAGGACGA CGGCAACTAC AAGACCCGCG CCGAGGTGAA
- TTCCGATGCA GGTCCTCGCG TGGTAGAAGA AGTTCCTGCT GCCGTTGATG TTCTGGGCGC GGCTCCACTT
- 351 GTTCGAGGGC GACACCCTGG TGAACCGCAT CGAGCTGAAG GGCATCGACT TCAAGGAGGA CGGCAACATC
- ${\tt CAAGCTCCCG\ CTGTGGGACC\ ACTTGGCGTA\ GCTCGACTTC\ CCGTAGCTGA}$   ${\tt AGTTCCTCCT\ GCCGTTGTAG}$
- 421 CTGGGGCACA AGCTGGAGTA CAACTACAAC AGCCACAACG TCTATATCAT GGCCGACAAG CAGAAGAACG
- GACCCCGTGT TCGACCTCAT GTTGATGTTG TCGGTGTTGC AGATATAGTA
- 491 GCATCAAGGT GAACTTCAAG ATCCGCCACA ACATCGAGGA CGGCAGCGTG CAGCTCGCCG ACCACTACCA
- CGTAGTTCCA CTTGAAGTTC TAGGCGGTGT TGTAGCTCCT GCCGTCGCAC GTCGAGCGGC TGGTGATGGT
- 561 GCAGAACACC CCCATCGGCG ACGGCCCCGT GCTGCTGCCC GACAACCACT ACCTGAGCAC CCAGTCCGCC
- CGTCTTGTGG GGGTAGCCGC TGCCGGGGCA CGACGACGGG CTGTTGGTGA TGGACTCGTG GGTCAGGCGG
- 631 CTGAGCAAAG ACCCCAACGA GAAGCGCGAT CACATGGTCC TGCTGGAGTT CGTGACCGCC GCCGGGATCA

Fig. 45B

CCGCATTATC GCTTCTCCGG GCGTGGCTAG CGGGAAGGGT TGTCAACGCG TCGGACTTAC CGCTTACCCT

1261 CGCGCCCTGT AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGCGCA GCGTGACCGC TACACTTGCC

GCGCGGGACA TCGCCGCGTA ATTCGCGCCG CCCACACCAC CAATGCGCGT CGCACTGGCG ATGTGAACGG

1331 AGCGCCCTAG CGCCCGCTCC TTTCGCTTTC TTCCCTTCCT TTCTCGCCAC GTTCGCCGGC TTTCCCCGTC

TCGCGGGATC GCGGGCGAGG AAAGCGAAAG AAGGGAAGGA AAGAGCGGTG

1401 AAGCTCTAAA TCGGGGGCTC CCTTTAGGGT TCCGATTTAG TGCTTTACGG CACCTCGACC CCAAAAAACT

 ${\tt TTCGAGATTT\ AGCCCCCGAG\ GGAAATCCCA\ AGGCTAAATC\ ACGAAATGCC\ GTGGAGCTGG\ GGTTTTTTGA}$ 

1471 TGATTAGGGT GATGGTTCAC GTAGTGGGCC ATCGCCCTGA TAGACGGTTT TTCGCCCTTT GACGTTGGAG

ACTAATCCCA CTACCAAGTG CATCACCCGG TAGCGGGACT ATCTGCCAAA AAGCGGGAAA CTGCAACCTC

1541 TCCACGTTCT TTAATAGTGG ACTCTTGTTC CAAACTGGAA CAACACTCAA

AGGTGCAAGA AATTATCACC TGAGAACAAG GTTTGACCTT GTTGTGAGTT GGGATAGAGC CAGATAAGAA

1611 TTGATTTATA AGGGATTTTG CCGATTTCGG CCTATTGGTT AAAAAATGAG CTGATTTAAC AAAAATTTAA

AACTAAATAT TCCCTAAAAC GGCTAAAGCC GGATAACCAA TTTTTTACTC GACTAAATTG TTTTTAAATT

1681 CGCGAATTTT AACAAAATAT TAACGCTTAC AATTTAGGTG GCACTTTTCG GGGAAATGTG CGCGGAACCC

GCGCTTAAAA TTGTTTTATA ATTGCGAATG TTAAATCCAC CGTGAAAAGC CCCTTTACAC GCGCCTTGGG

1751 CTATTTGTTT ATTTTTCTAA ATACATTCAA ATATGTATCC GCTCATGAGA CAATAACCCT GATAAATGCT

GATAACAAA TAAAAAGATT TATGTAAGTT TATACATAGG CGAGTACTCT GTTATTGGGA CTATTTACGA

1821 TCAATAATAT TGAAAAAGGA AGAGTATGAG TATTCAACAT TTCCGTGTCG CCCTTATTCC CTTTTTTGCG

AGTTATTATA ACTTTTTCCT TCTCATACTC ATAAGTTGTA AAGGCACAGC GGGAATAAGG GAAAAAACGC

1891 GCATTTTGCC TTCCTGTTTT TGCTCACCCA GAAACGCTGG TGAAAGTAAA AGATGCTGAA GATCAGTTGG

CGTAAAACGG AAGGACAAAA ACGAGTGGGT CTTTGCGACC ACTTTCATTT TCTACGACTT CTAGTCAACC

Fig. 45 C

1961 GTGCACGAGT GGGTTACATC GAACTGGATC TCAACAGCGG TAAGATCCTT GAGAGTTTTC GCCCCGAAGA

CACGTGCTCA CCCAATGTAG CTTGACCTAG AGTTGTCGCC ATTCTAGGAA

2031 ACGTTTTCCA ATGATGAGCA CTTTTAAAGT TCTGCTATGT GGCGCGGTAT TATCCCGTAT TGACGCCGGG

TGCAAAAGGT TACTACTCGT GAAAATTTCA AGACGATACA CCGCGCCATA
ATAGGGCATA ACTGCGGCCC

2101 CAAGAGCAAC TCGGTCGCCG CATACACTAT TCTCAGAATG ACTTGGTTGA GTACTCACCA GTCACAGAAA

GTTCTCGTTG AGCCAGCGGC GTATGTGATA AGAGTCTTAC TGAACCAACT CATGAGTGGT CAGTGTCTTT

2171 AGCATCTTAC GGATGGCATG ACAGTAAGAG AATTATGCAG TGCTGCCATA ACCATGAGTG ATAACACTGC

TCGTAGAATG CCTACCGTAC TGTCATTCTC TTAATACGTC ACGACGGTAT TGGTACTCAC TATTGTGACG

2241 GGCCAACTTA CTTCTGACAA CGATCGGAGG ACCGAAGGAG CTAACCGCTT

2311 CATGTAACTC GCCTTGATCG TTGGGAACCG GAGCTGAATG AAGCCATACC AAACGACGAG CGTGACACCA

GTACATTGAG CGGAACTAGC AACCCTTGGC CTCGACTTAC TTCGGTATGG
TTTGCTGCTC GCACTGTGGT

2381 CGATGCCTGT AGCAATGGCA ACAACGTTGC GCAAACTATT AACTGGCGAA

GCTACGGACA TCGTTACCGT TGTTGCAACG CGTTTGATAA TTGACCGCTT GATGAATGAG ATCGAAGGGC

2451 GCAACAATTA ATAGACTGGA TGGAGGCGGA TAAAGTTGCA GGACCACTTC TGCGCTCGGC CCTTCCGGCT

CGTTGTTAAT TATCTGACCT ACCTCCGCCT ATTTCAACGT CCTGGTGAAG ACGCGAGCCG GGAAGGCCGA

2521 GGCTGGTTTA TTGCTGATAA ATCTGGAGCC GGTGAGCGTG GGTCTCGCGG
TATCATTGCA GCACTGGGGC

CCGACCAAAT AACGACTATT TAGACCTCGG CCACTCGCAC CCAGAGCGCC ATAGTAACGT CGTGACCCCG

2591 CAGATGGTAA GCCCTCCCGT ATCGTAGTTA TCTACACGAC GGGGAGTCAG GCAACTATGG ATGAACGAAA

GTCTACCATT CGGGAGGGCA TAGCATCAAT AGATGTGCTG CCCCTCAGTC CGTTGATACC TACTTGCTTT

2661 TAGACAGATC GCTGAGATAG GTGCCTCACT GATTAAGCAT TGGTAACTGT CAGACCAAGT TTACTCATAT

ATCTGTCTAG CGACTCTATC CACGGAGTGA CTAATTCGTA ACCATTGACA GTCTGGTTCA AATGAGTATA

- 2731 ATACTTTAGA TTGATTTAAA ACTTCATTTT TAATTTAAAA GGATCTAGGT
  GAAGATCCTT TTTGATAATC
- TATGAAATCT AACTAAATTT TGAAGTAAAA ATTAAATTTT CCTAGATCCA
- 2801 TCATGACCAA AATCCCTTAA CGTGAGTTTT CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG
- AGTACTGGTT TTAGGGAATT GCACTCAAAA GCAAGGTGAC TCGCAGTCTG
- 2871 ATCTTCTTGA GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG
- TAGAAGAACT CTAGGAAAAA AAGACGCGCA TTAGACGACG AACGTTTGTT
- 2941 GTGGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC AGAGCGCAGA
- CACCAAACAA ACGGCCTAGT TCTCGATGGT TGAGAAAAAG GCTTCCATTG ACCGAAGTCG TCTCGCGTCT
- 3011 TACCAAATAC TGTCCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG AACTCTGTAG CACCGCCTAC
- ATGGTTTATG ACAGGAAGAT CACATCGGCA TCAATCCGGT GGTGAAGTTC TTGAGACATC GTGGCGGATG
- 3081 ATACCTCGCT CTGCTAATCC TGTTACCAGT GGCTGCTGCC AGTGGCGATA AGTCGTGTCT TACCGGGTTG
- TATGGAGCGA GACGATTAGG ACAATGGTCA CCGACGACGG TCACCGCTAT TCAGCACAGA ATGGCCCAAC
- 3151 GACTCAAGAC GATAGTTACC GGATAAGGCG CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA
- CTGAGTTCTG CTATCAATGG CCTATTCCGC GTCGCCAGCC CGACTTGCCC CCCAAGCACG TGTGTCGGGT
- 3221 GCTTGGAGCG AACGACCTAC ACCGAACTGA GATACCTACA GCGTGAGCTA
  TGAGAAAGCG CCACGCTTCC
- CGAACCTCGC TTGCTGGATG TGGCTTGACT CTATGGATGT CGCACTCGAT ACTCTTTCGC GGTGCGAAGG
- 3291 CGAAGGGAGA AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC GAGGGAGCTT
- 3361 CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCGGGT TTCGCCACCT
- GGTCCCCCTT TGCGGACCAT AGAAATATCA GGACAGCCCA AAGCGGTGGA GACTGAACTC GCAGCTAAAA
- 3431 TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG GCCTTTTTAC GGTTCCTGGC

ACACTACGAG CAGTCCCCCC GCCTCGGATA CCTTTTTGCG GTCGTTGCGC CGGAAAAATG CCAAGGACCG

3501 CTTTTGCTG CCTTTTGCTC ACATGTTCTT TCCTGCGTTA TCCCCTGATT CTGTGGATAA CCGTATTACC

GAAAACGACC GGAAAACGAG TGTACAAGAA AGGACGCAAT AGGGGACTAA GACACCTATT GGCATAATGG

3571 GCCTTTGAGT GAGCTGATAC CGCTCGCCGC AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG

CGGAAACTCA CTCGACTATG GCGAGCGGCG TCGGCTTGCT GGCTCGCGTC

3641 CGGAAGAGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG TTGGCCGATT CATTAATGCA GCTGGCACGA

GCCTTCTCGC GGGTTATGCG TTTGGCGGAG AGGGGCGCGC AACCGGCTAA

3711 CAGGTTTCCC GACTGGAAAG CGGGCAGTGA GCGCAACGCA ATTAATGTGA GTTAGCTCAC TCATTAGGCA

GTCCAAAGGG CTGACCTTTC GCCCGTCACT CGCGTTGCGT TAATTACACT CAATCGAGTG AGTAATCCGT

3781 CCCCAGGCTT TACACTTTAT GCTTCCGGCT CGTATGTTGT GTGGAATTGT GAGCGGATAA CAATTTCACA

GGGGTCCGAA ATGTGAAATA CGAAGGCCGA GCATACAACA CACCTTAACA

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3851 CAGGAAACAG CTATGACCAT GATTACGCCA AGCGCGCAAT TAACCCTCAC TAAAGGGAAC AAAAGCTGGG

 ${\tt GTCCTTGTC} \ \ {\tt GATACTGGTA} \ \ {\tt CTAATGCGGT} \ \ {\tt TCGCGCGTTA} \ \ {\tt ATTGGGAGTG}$   ${\tt ATTTCCCTTG} \ \ {\tt TTTTCGACCC}$ 

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3921 TACCGGGCCC CCCCTCGAGG TCATTCATAT GCTTGAGAAG AGAGTCGGGA TAGTCCAAAA TAAAACAAAG

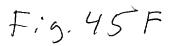
ATGGCCCGGG GGGGAGCTCC AGTAAGTATA CGAACTCTTC TCTCAGCCCT

3991 GTAAGATTAC CTGGTCAAAA GTGAAAACAT CAGTTAAAAG GTGGTATAAG TAAAATATCG GTAATAAAAG

 $\hbox{ CATTCTAATG GACCAGTTTT CACTTTTGTA GTCAATTTC CACCATATTC} \\ \hbox{ATTTTATAGC CATTATTTC}$ 

4061 GTGGCCCAAA GTGAAATTTA CTCTTTTCTA CTATTATAAA AATTGAGGAT GTTTTGTCGG TACTTTGATA

CACCGGGTTT CACTTTAAAT GAGAAAAGAT GATAATATTT TTAACTCCTA



4131 CGTCATTTT GTATGAATTG GTTTTTAAGT TTATTCGCGA TTTGGAAATG CATATCTGTA TTTGAGTCGG

GCAGTAAAAA CATACTTAAC CAAAAATTCA AATAAGCGCT AAACCTTTAC
GTATAGACAT AAACTCAGCC

4201 TTTTTAAGTT CGTTGCTTTT GTAAATACAG AGGGATTTGT ATAAGAAATA
TCTTTAAAAA ACCCATATGC

AAAAATTCAA GCAACGAAAA CATTTATGTC TCCCTAAACA TATTCTTTAT

EcoRI

4271 TAATTTGACA TAATTTTTGA GAAAAATATA TATTCAGGCG AATTCCACAA TGAACAATAA TAAGATTAAA

ATTAAACTGT ATTAAAAACT CTTTTTATAT ATAAGTCCGC TTAAGGTGTT
ACTTGTTATT ATTCTAATTT

4341 ATAGCTTGCC CCCGTTGCAG CGATGGGTAT TTTTTCTAGT AAAATAAAAG ATAAACTTAG ACTCAAAACA

TATCGAACGG GGGCAACGTC GCTACCCATA AAAAAGATCA TTTTATTTTC
TATTTGAATC TGAGTTTTGT

4411 TTTACAAAAA CAACCCCTAA AGTCCTAAAG CCCAAAGTGC TATGCACGAT CCATAGCAAG CCCAGCCCAA

AAATGTTTTT GTTGGGGATT TCAGGATTTC GGGTTTCACG ATACGTGCTA

4481 CCCAACCCAA CCCAACCCAC CCCAGTGCAG CCAACTGGCA AATAGTCTCC ACCCCGGCA CTATCACCGT

 ${\tt GGGTTGGGTT~GGGTG~GGGTCACGTC~GGTTGACCGT~TTATCAGAGG~TGGGGGCCGT~GATAGTGGCA}$ 

4621 CAGCAGGTGG GTCCGGGTCG TGGGGGCCGG AAAAGCGAGG AGGATCGCGA GCAGCGACGA GGCCCGGCCC

GTCGTCCACC CAGGCCCAGC ACCCCCGGCC TTTTCGCTCC TCCTAGCGCT

4691 TCCCTCCGCT TCCAAAGAAA CGCCCCCCAT CGCCACTATA TACATACCCC

AGGGAGGCGA AGGTTTCTTT GCGGGGGGTA GCGGTGATAT ATGTATGGGG

4761 CAACCCTACC ACCACCACCA CCACCACCTC CTCCCCCCTC GCTGCCGGAC GACGAGCTCC TCCCCCCTCC

GTTGGGATGG TGGTGGTGGT GGTGGTGGAG GAGGGGGAG CGACGGCCTG

 $4831 \quad \texttt{CCCTCCGCCG} \quad \texttt{CCGCCGGTAA} \quad \texttt{CCACCCCGCC} \quad \texttt{CCTCTCCTCT} \quad \texttt{TTCTTTCTCC} \\ \texttt{GTTTTTTTT} \quad \texttt{TCGTCTCGGT}$ 

Fig. 45 G

 ${\tt GGGAGGCGGC\ GGCGGCCATT\ GGTGGGGCGG\ GGAGAGGAGA\ AAGAAAAAGAGGCCA}$   ${\tt CAAAAAAAAAA\ AGCAGAGCCA}$ 

4901 CTCGATCTTT GGCCTTGGTA GTTTGGGTGG GCGAGAGCGG CTTCGTCGCC CAGATCGGTG CGCGGGAGGG

GAGCTAGAAA CCGGAACCAT CAAACCCACC CGCTCTCGCC GAAGCAGCGG

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4971 GCGGGATCTC GCGGCTGGCG TCTCCGGGCG TGAGTCGGCC CGGATCCTCG CGGGGAATGG GGCTCTCGGA

CGCCCTAGAG CGCCGACCGC AGAGGCCCGC ACTCAGCCGG GCCTAGGAGC GCCCCTTACC CCGAGAGCCT

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5041 TGTAGATCTT CTTTCTTTCT TCTTTTTGTG GTAGAATTTG AATCCCTCAG CATTGTTCAT CGGTAGTTTT

ACATCTAGAA GAAAGAAAGA AGAAAAACAC CATCTTAAAC TTAGGGAGTC GTAACAAGTA GCCATCAAAA

5111 TCTTTTCATG ATTTGTGACA AATGCAGCCT CGTGCGGAGC TTTTTTGTAG GTAG AGAAAAGTAC TAAACACTGT TTACGTCGGA GCACGCCTCG AAAAAACATC CATC

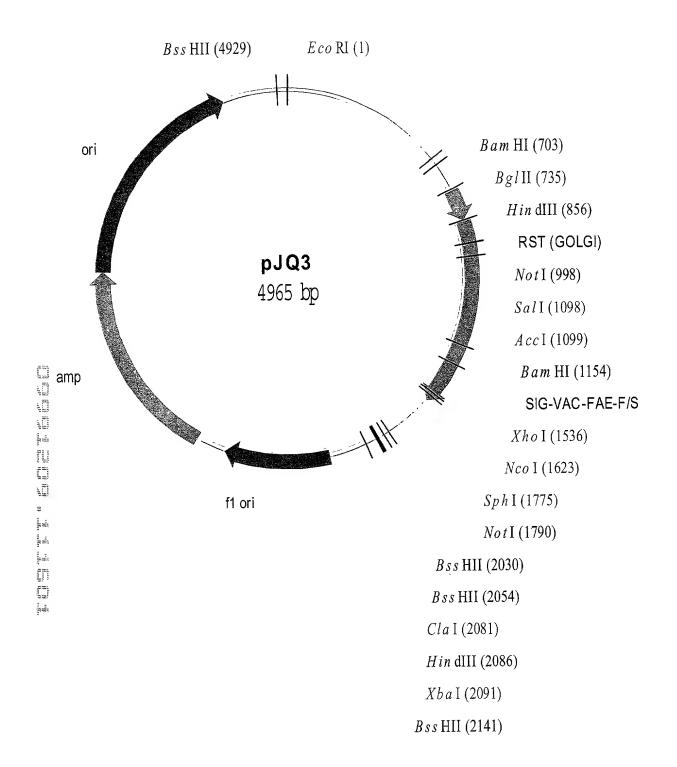


Fig. 46A

### Sequence for pJQ3

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1 AATTCCACAA TGAACAATAA TAAGATTAAA ATAGCTTGCC CCCGTTGCAG CGATGGGTAT TTTTTCTAGT TTAAGGTGTT ACTTGTTATT ATTCTAATTT TATCGAACGG GGGCAACGTC

TTAAGGTGTT ACTTGTTATT ATTCTAATTT TATCGAACGG GGGCAACGTC GCTACCCATA AAAAAGATCA

71 AAAATAAAAG ATAAACTTAG ACTCAAAACA TTTACAAAAA CAACCCCTAA
AGTCCTAAAG CCCAAAGTGC

TTTTATTTTC TATTTGAATC TGAGTTTTGT AAATGTTTTT GTTGGGGATT TCAGGATTTC GGGTTTCACG

211 AATAGTCTCC ACCCCCGGCA CTATCACCGT GAGTTGTCCG CACCACCGCA

TTATCAGAGG TGGGGGCCGT GATAGTGGCA CTCAACAGGC GTGGTGGCGT GCAGAGCGTC GGTTTTTTTT

281 AAAAAGAAAG AAAAAAAAAA AAAAGAAAAA CAGCAGGTGG GTCCGGGTCG TGGGGGCCGG AAAAGCGAGG

TTTTTCTTTC TTTTTTTCT TTTTCTTTTT GTCGTCCACC CAGGCCCAGC ACCCCCGGCC TTTTCGCTCC

351 AGGATCGCGA GCAGCGACGA GGCCCGGCCC TCCCTCCGCT TCCAAAGAAA

TCCTAGCGCT CGTCGCTGCT CCGGGCCGGG AGGGAGGCGA AGGTTTCTTT
GCGGGGGGTA GCGGTGATAT

421 TACATACCCC CCCCTCTCCT CCCATCCCCC CAACCCTACC ACCACCACCA

ATGTATGGGG GGGGAGAGGA GGGTAGGGGG GTTGGGATGG TGGTGGTGGT GGTGGTGGAG GAGGGGGGAG

491 GCTGCCGGAC GACGAGCTCC TCCCCCCTCC CCCTCCGCCG CCGCCGGTAA

561 TTCTTTCTCC GTTTTTTTT TCGTCTCGGT CTCGATCTTT GGCCTTGGTA GTTTGGGTGG GCGAGAGCGG

AAGAAAGAGG CAAAAAAAA AGCAGAGCCA GAGCTAGAAA CCGGAACCAT

631 CTTCGTCGCC CAGATCGGTG CGCGGGAGGG GCGGGATCTC GCGGCTGGCG TCTCCGGGCG TGAGTCGGCC

Fig. 46 B

GAAGCAGCGG GTCTAGCCAC GCGCCCTCCC CGCCCTAGAG CGCCGACCGC AGAGGCCCGC ACTCAGCCGG

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701 CGGATCCTCG CGGGGAATGG GGCTCTCGGA TGTAGATCTT CTTTCTTTCT TCTTTTTGTG GTAGAATTTG

GCCTAGGAGC GCCCCTTACC CCGAGAGCCT ACATCTAGAA GAAAGAAAGA AGAAAAACAC CATCTTAAAC

771 AATCCCTCAG CATTGTTCAT CGGTAGTTTT TCTTTTCATG ATTTGTGACA
AATGCAGCCT CGTGCGGAGC

TTAGGGAGTC GTAACAAGTA GCCATCAAAA AGAAAAGTAC TAAACACTGT TTACGTCGGA GCACGCCTCG

#### HindIII

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841 TTTTTGTAG GTAGAAGCTT ACCATGATCC ACACCAACCT CAAAAAGAAG
TTCTCCCTCT TCATCCTCGT

AAAAAACATC CATCTTCGAA TGGTACTAGG TGTGGTTGGA GTTTTTCTTC AAGAGGGAGA AGTAGGAGCA

911 CTTCCTCCT TTCGCCGTGA TCTGCGTGTG GAAGAAGGGC TCCGACTACG AGGCCCTCAC CCTCCAAGCC

GAAGGAGGA AAGCGGCACT AGACGCACAC CTTCTTCCCG AGGCTGATGC TCCGGGAGTG GGAGGTTCGG

#### NotI

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981 AAGGAGTTCC AAATGGCGGC CGCCTCCACG CAGGGCATCT CCGAAGACCT CTACAGCCGT TTAGTCGAAA

TTCCTCAAGG TTTACCGCCG GCGGAGGTGC GTCCCGTAGA GGCTTCTGGA GATGTCGGCA AATCAGCTTT

SalI

Acct

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1051 TGGCCACTAT CTCCCAAGCT GCCTACGCCG ACCTGTGCAA CATTCCGTCG ACTATTATCA AGGGAGAGAA

ACCGGTGATA GAGGGTTCGA CGGATGCGGC TGGACACGTT GTAAGGCAGC TGATAATAGT TCCCTCTCTT

### BamHI

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1121 AATTTACAAT TCTCAAACTG ACATTAACGG ATGGATCCTC CGCGACGACA GCAGCAAAGA AATAATCACC

TTAAATGTTA AGAGTTTGAC TGTAATTGCC TACCTAGGAG GCGCTGCTGT CGTCGTTTCT TTATTAGTGG

1191 GTCTTCCGTG GCACTGGTAG TGATACGAAT CTACAACTCG ATACTAACTA CACCCTCACG CCTTTCGACA

CAGAAGGCAC CGTGACCATC ACTATGCTTA GATGTTGAGC TATGATTGAT GTGGGAGTGC GGAAAGCTGT

Fig. 46 C

1261 CCCTACCACA ATGCAACGGT TGTGAAGTAC ACGGTGGATA TTATATTGGA TGGGTCTCCG TCCAGGACCA

GGGATGGTGT TACGTTGCCA ACACTTCATG TGCCACCTAT AATATAACCT ACCCAGAGGC AGGTCCTGGT

1331 AGTCGAGTCG CTTGTCAAAC AGCAGGTTAG CCAGTATCCG GACTACGCGC TGACCGTGAC CGGCCACKCC

TCAGCTCAGC GAACAGTTTG TCGTCCAATC GGTCATAGGC CTGATGCGCG ACTGGCACTG GCCGGTGMGG

1401 CTCGGCGCCT CCCTGGCGGC ACTCACTGCC GCCCAGCTGT CTGCGACATA CGACAACATC CGCCTGTACA

GAGCCGCGGA GGGACCGCCG TGAGTGACGG CGGGTCGACA GACGCTGTAT GCTGTTGTAG GCGGACATGT

XhoI

1471 CCTTCGGCGA ACCGCGCAGC GGCAATCAGG CCTTCGCGTC GTACATGAAC GATGCCTTCC AAGCCTCGAG

GGAAGCCGCT TGGCGCGTCG CCGTTAGTCC GGAAGCGCAG CATGTACTTG

1541 CCCAGATACG ACGCAGTATT TCCGGGTCAC TCATGCCAAC GACGGCATCC CAAACCTGCC CCCGGTGGAG

GGGTCTATGC TGCGTCATAA AGGCCCAGTG AGTACGGTTG CTGCCGTAGG

### NcoI

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1611 CAGGGGTACG CCCATGGCGG TGTAGAGTAC TGGAGCGTTG ATCCTTACAG CGCCAGAAC ACATTGTCT

 ${\tt GTCCCCATGC~GGGTACCGCC~ACATCTCATG~ACCTCGCAAC~TAGGAATGTC}\\ {\tt GCGGGTCTTG~TGTAAACAGA}\\$ 

1681 GCACTGGGGA TGAAGTGCAG TGCTGTGAGG CCCAGGGCGG ACAGGGTGTG
AATAATGCGC ACACGACTTA

CGTGACCCCT ACTTCACGTC ACGACACTCC GGGTCCCGCC TGTCCCACAC TTATTACGCG TGTGCTGAAT

SphI

NotI

1751 TTTTGGGATG ACGAGCGGCG CATGCACCTG GCCGGTCGCG GCCGCGGAAA CCACTGAAGG ATGAGCTGTA

AAAACCCTAC TGCTCGCCGC GTACGTGGAC CGGCCAGCGC CGGCGCCTTT GGTGACTTCC TACTCGACAT

1821 AAGAAGCAGA TCGTTCAAAC ATTTGGCAAT AAAGTTTCTT AAGATTGAAT CCTGTTGCCG GTCTTGCGAT

TTCTTCGTCT AGCAAGTTTG TAAACCGTTA TTTCAAAGAA TTCTAACTTA GGACAACGGC CAGAACGCTA

Fig. 46 D

1891 GATTATCATA TAATTTCTGT TGAATTACGT TAAGCATGTA ATAATTAACA TGTAATGCAT GACGTTATTT

CTAATAGTAT ATTAAAGACA ACTTAATGCA ATTCGTACAT TATTAATTGT ACATTACGTA CTGCAATAAA

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1961 ATGAGATGGG TTTTTATGAT TAGAGTCCCG CAATTATACA TTTAATACGC GATAGAAAAC AAAATATAGC

TACTCTACCC AAAAATACTA ATCTCAGGGC GTTAATATGT AAATTATGCG

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| ADa | Τ |

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2031 GCGCAAACTA GGATAAATTA TCGCGCGCGG TGTCATCTAT GTTACTAGAT CGATAAGCTT CTAGAGCGGC

CGCGTTTGAT CCTATTTAAT AGCGCGCGCC ACAGTAGATA CAATGATCTA

#### BssHII

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2101 CGGTGGAGCT CCAATTCGCC CTATAGTGAG TCGTATTACG CGCGCTCACT GGCCGTCGTT TTACAACGTC

GCCACCTCGA GGTTAAGCGG GATATCACTC AGCATAATGC GCGCGAGTGA

2171 GTGACTGGGA AAACCCTGGC GTTACCCAAC TTAATCGCCT TGCAGCACAT CCCCCTTTCG CCAGCTGGCG

CACTGACCCT TTTGGGACCG CAATGGGTTG AATTAGCGGA ACGTCGTGTA GGGGGAAAGC GGTCGACCGC

2241 TAATAGCGAA GAGGCCCGCA CCGATCGCCC TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGGACGCG

ATTATCGCTT CTCCGGGCGT GGCTAGCGGG AAGGGTTGTC AACGCGTCGG ACTTACCGCT TACCCTGCGC

2311 CCCTGTAGCG GCGCATTAAG CGCGGCGGGT GTGGTGGTTA CGCGCAGCGT GACCGCTACA CTTGCCAGCG

GGGACATCGC CGCGTAATTC GCGCCGCCCA CACCACCAAT GCGCGTCGCA CTGGCGATGT GAACGGTCGC

2381 CCCTAGCGCC CGCTCCTTTC GCTTTCTTCC CTTCCTTTCT CGCCACGTTC GCCGGCTTTC CCCGTCAAGC

GGGATCGCGG GCGAGGAAAG CGAAAGAAGG GAAGGAAAGA GCGGTGCAAG

2451 TCTAAATCGG GGGCTCCCTT TAGGGTTCCG ATTTAGTGCT TTACGGCACC TCGACCCCAA AAAACTTGAT

AGATTTAGCC CCCGAGGGAA ATCCCAAGGC TAAATCACGA AATGCCGTGG AGCTGGGGTT TTTTGAACTA

2521 TAGGGTGATG GTTCACGTAG TGGGCCATCG CCCTGATAGA CGGTTTTTCG CCCTTTGACG TTGGAGTCCA

ATCCCACTAC CAAGTGCATC ACCCGGTAGC GGGACTATCT GCCAAAAAGC GGGAAACTGC AACCTCAGGT

2591 CGTTCTTTAA TAGTGGACTC TTGTTCCAAA CTGGAACAAC ACTCAACCCT ATCTCGGTCT ATTCTTTTGA

GCAAGAAATT ATCACCTGAG AACAAGGTTT GACCTTGTTG TGAGTTGGGA TAAGAAAACT

2661 TTTATAAGGG ATTTTGCCGA TTTCGGCCTA TTGGTTAAAA AATGAGCTGA TTTAACAAAA ATTTAACGCG

AAATATTCCC TAAAACGGCT AAAGCCGGAT AACCAATTTT TTACTCGACT AAATTGTTTT TAAATTGCGC

2731 AATTTTAACA AAATATTAAC GCTTACAATT TAGGTGGCAC TTTTCGGGGA AATGTGCGCG GAACCCCTAT

TTAAAATTGT TTTATAATTG CGAATGTTAA ATCCACCGTG AAAAGCCCCT

2801 TTGTTTATTT TTCTAAATAC ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCCTGATA AATGCTTCAA

AACAAATAAA AAGATTTATG TAAGTTTATA CATAGGCGAG TACTCTGTTA

2871 TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC GTGTCGCCCT TATTCCCTTT TTTGCGGCAT

ATTATAACTT TTTCCTTCTC ATACTCATAA GTTGTAAAGG CACAGCGGGA ATAAGGGAAA AAACGCCGTA

2941 TTTGCCTTCC TGTTTTTGCT CACCCAGAAA CGCTGGTGAA AGTAAAAGAT GCTGAAGATC AGTTGGGTGC

AAACGGAAGG ACAAAAACGA GTGGGTCTTT GCGACCACTT TCATTTTCTA CGACTTCTAG TCAACCCACG

3011 ACGAGTGGGT TACATCGAAC TGGATCTCAA CAGCGGTAAG ATCCTTGAGAGTTTTCGCCC CGAAGAACGT

TGCTCACCCA ATGTAGCTTG ACCTAGAGTT GTCGCCATTC TAGGAACTCT CAAAAGCGGG GCTTCTTGCA

3081 TTTCCAATGA TGAGCACTTT TAAAGTTCTG CTATGTGGCG CGGTATTATC CCGTATTGAC GCCGGGCAAG

AAAGGTTACT ACTCGTGAAA ATTTCAAGAC GATACACCGC GCCATAATAG GGCATAACTG CGGCCCGTTC

3151 AGCAACTCGG TCGCCGCATA CACTATTCTC AGAATGACTT GGTTGAGTAC TCACCAGTCA CAGAAAAGCA

TCGTTGAGCC AGCGGCGTAT GTGATAAGAG TCTTACTGAA CCAACTCATG AGTGGTCAGT GTCTTTTCGT

- 3221 TCTTACGGAT GGCATGACAG TAAGAGAATT ATGCAGTGCT GCCATAACCA TGAGTGATAA CACTGCGGCC
- AGAATGCCTA CCGTACTGTC ATTCTCTTAA TACGTCACGA CGGTATTGGT ACTCACTATT GTGACGCCGG
- 3291 AACTTACTTC TGACAACGAT CGGAGGACCG AAGGAGCTAA CCGCTTTTTT GCACAACATG GGGGATCATG
- TTGAATGAAG ACTGTTGCTA GCCTCCTGGC TTCCTCGATT GGCGAAAAAA CGTGTTGTAC CCCCTAGTAC
- 3361 TAACTCGCCT TGATCGTTGG GAACCGGAGC TGAATGAAGC CATACCAAAC GACGAGCGTG ACACCACGAT
- ATTGAGCGGA ACTAGCAACC CTTGGCCTCG ACTTACTTCG GTATGGTTTG
- 3431 GCCTGTAGCA ATGGCAACAA CGTTGCGCAA ACTATTAACT GGCGAACTAC TTACTCTAGC TTCCCGGCAA
- 3501 CAATTAATAG ACTGGATGGA GGCGGATAAA GTTGCAGGAC CACTTCTGCG
- GTTAATTATC TGACCTACCT CCGCCTATTT CAACGTCCTG GTGAAGACGC GAGCCGGGAA GGCCGACCGA
- 3571 GGTTTATTGC TGATAAATCT GGAGCCGGTG AGCGTGGGTC TCGCGGTATC ATTGCAGCAC TGGGGCCAGA
- CCAAATAACG ACTATTTAGA CCTCGGCCAC TCGCACCCAG AGCGCCATAG TAACGTCGTG ACCCCGGTCT
- 3641 TGGTAAGCCC TCCCGTATCG TAGTTATCTA CACGACGGGG AGTCAGGCAA CTATGGATGA ACGAAATAGA
- ACCATTCGGG AGGGCATAGC ATCAATAGAT GTGCTGCCCC TCAGTCCGTT GATACCTACT TGCTTTATCT
- 3711 CAGATCGCTG AGATAGGTGC CTCACTGATT AAGCATTGGT AACTGTCAGA CCAAGTTTAC TCATATATAC
- GTCTAGCGAC TCTATCCACG GAGTGACTAA TTCGTAACCA TTGACAGTCT GGTTCAAATG AGTATATATG
- 3781 TTTAGATTGA TTTAAAACTT CATTTTTAAT TTAAAAGGAT CTAGGTGAAG ATCCTTTTTG ATAATCTCAT
- AAATCTAACT AAATTTTGAA GTAAAAATTA AATTTTCCTA GATCCACTTC TAGGAAAAAC TATTAGAGTA
- 3851 GACCAAAATC CCTTAACGTG AGTTTTCGTT CCACTGAGCG TCAGACCCCG
  TAGAAAAGAT CAAAGGATCT
- CTGGTTTTAG GGAATTGCAC TCAAAAGCAA GGTGACTCGC AGTCTGGGGC ATCTTTCTA GTTTCCTAGA
- 3921 TCTTGAGATC CTTTTTTCT GCGCGTAATC TGCTGCTTGC AAACAAAAA ACCACCGCTA CCAGCGGTGG

AGAACTCTAG GAAAAAAAGA CGCGCATTAG ACGACGAACG TTTGTTTTTTTGGTGGCGAT GGTCGCCACC

3991 TTTGTTTGCC GGATCAAGAG CTACCAACTC TTTTTCCGAA GGTAACTGGC TTCAGCAGAG CGCAGATACC

AAACAAACGG CCTAGTTCTC GATGGTTGAG AAAAAGGCTT CCATTGACCG AAGTCGTCTC GCGTCTATGG

- 4061 AAATACTGTC CTTCTAGTGT AGCCGTAGTT AGGCCACCAC TTCAAGAACT CTGTAGCACC GCCTACATAC
- TTTATGACAG GAAGATCACA TCGGCATCAA TCCGGTGGTG AAGTTCTTGA GACATCGTGG CGGATGTATG
- 4131 CTCGCTCTGC TAATCCTGTT ACCAGTGGCT GCTGCCAGTG GCGATAAGTC
- GAGCGAGACG ATTAGGACAA TGGTCACCGA CGACGGTCAC CGCTATTCAG CACAGAATGG CCCAACCTGA
- 4201 CAAGACGATA GTTACCGGAT AAGGCGCAGC GGTCGGGCTG AACGGGGGGT TCGTGCACAC AGCCCAGCTT
- GTTCTGCTAT CAATGGCCTA TTCCGCGTCG CCAGCCCGAC TTGCCCCCCA AGCACGTGTG TCGGGTCGAA
- 4271 GGAGCGAACG ACCTACACCG AACTGAGATA CCTACAGCGT GAGCTATGAG AAAGCGCCAC GCTTCCCGAA
- CCTCGCTTGC TGGATGTGGC TTGACTCTAT GGATGTCGCA CTCGATACTC
- 4341 GGGAGAAAGG CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA GCGCACGAGG GAGCTTCCAG
- CCCTCTTTCC GCCTGTCCAT AGGCCATTCG CCGTCCCAGC CTTGTCCTCT
- 4411 GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA
- CCCCTTTGCG GACCATAGAA ATATCAGGAC AGCCCAAAGC GGTGGAGACT GAACTCGCAG CTAAAAAACAC
- 4481 ATGCTCGTCA GGGGGGCGGA GCCTATGGAA AAACGCCAGC AACGCGGCCT
- TACGAGCAGT CCCCCCCCCT CGGATACCTT TTTGCGGTCG TTGCGCCGGA AAAATGCCAA GGACCGGAAA
- 4551 TGCTGGCCTT TTGCTCACAT GTTCTTTCCT GCGTTATCCC CTGATTCTGT GGATAACCGT ATTACCGCCT
- ACGACCGGAA AACGAGTGTA CAAGAAAGGA CGCAATAGGG GACTAAGACA
- 4621 TTGAGTGAGC TGATACCGCT CGCCGCAGCC GAACGACCGA GCGCAGCGAG TCAGTGAGCG AGGAAGCGGA
- AACTCACTCG ACTATGGCGA GCGGCGTCGG CTTGCTGGCT CGCGTCGCTC AGTCACTCGC TCCTTCGCCT

- 4691 AGAGCGCCCA ATACGCAAAC CGCCTCTCCC CGCGCGTTGG CCGATTCATT AATGCAGCTG GCACGACAGG
- TCTCGCGGGT TATGCGTTTG GCGGAGAGGG GCGCGCAACC GGCTAAGTAA
  TTACGTCGAC CGTGCTGTCC
- 4761 TTTCCCGACT GGAAAGCGGG CAGTGAGCGC AACGCAATTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC
- AAAGGGCTGA CCTTTCGCCC GTCACTCGCG TTGCGTTAAT TACACTCAAT CGAGTGAGTA ATCCGTGGGG
- $4831\,$  AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC GGATAACAAT TTCACACAGG
- TCCGAAATGT GAAATACGAA GGCCGAGCAT ACAACACCC TTAACACTCG CCTATTGTTA AAGTGTGTCC

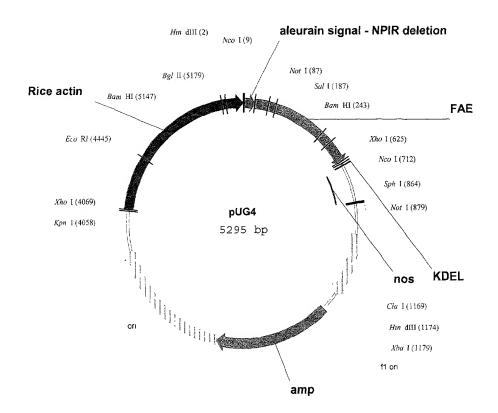
#### BssHII

EcoRI

4901 AAACAGCTAT GACCATGATT ACGCCAAGCG CGCAATTAAC CCTCACTAAA GGGAACAAAA GCTGG

TTTGTCGATA CTGGTACTAA TGCGGTTCGC GCGTTAATTG GGAGTGATTT CCCTTGTTTT CGACC

# Figure 47 A



1751

### Figure 473

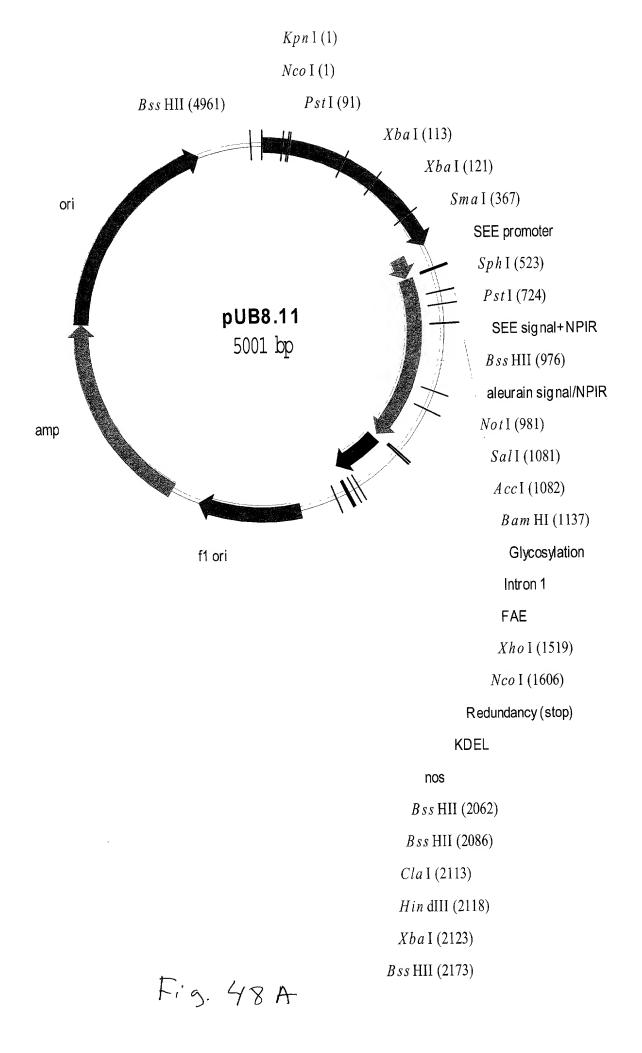
NCOT

HindIII M A H A R V L L L A L A V L A T A A V A V AAGCTTACCA TGGCCCACGC CCGCGTCCTC CTCCTGGCGC TCGCCGTGCT GGCCACGGCC GCCGTCGCCG Not.T · ASSRAAASTQGISEDLYSRL TCGCCTCCTC CCGCGCGGCC GCCTCCACGC AGGGCATCTC CGAAGACCTC TACAGCCGTT TAGTCGAAAT 71 SalI · A T I S Q A A Y A D L C N I P S T I I K G E K GGCCACTATC TCCCAAGCTG CCTACGCCGA CCTGTGCAAC ATTCCGTCGA CTATTATCAA GGGAGAGAAA 141 I Y N S Q T D I N G W I L R D D S S K E I I T V ATTTACAATT CTCAAACTGA CATTAACGGA TGGATCCTCC GCGACGACAG CAGCAAAGAA ATAATCACCG 211 · FRG TGS D T N L Q L D T N Y T L T P F D T · TCTTCCGTGG CACTGGTAGT GATACGAATC TACAACTCGA TACTAACTAC ACCCTCACGC CTTTCGACAC 281 · L P Q C N G C E V H G G Y Y I G W V S V Q D Q CCTACCACAA TGCAACGGTT GTGAAGTACA CGGTGGATAT TATATTGGAT GGGTCTCCGT CCAGGACCAA VESLVKQQVSQYPDYALTVTGHXL GTCGAGTCGC TTGTCAAACA GCAGGTTAGC CAGTATCCGG ACTACGCGCT GACCGTGACC GGCCACKCCC 421 · G A S L A A L T A A O L S A T Y D N I R L Y T · TCGGCGCCTC CCTGGCGGCA CTCACTGCCG CCCAGCTGTC TGCGACATAC GACAACATCC GCCTGTACAC XhoI · F G E P R S G N Q A F A S Y M N D A F Q A S S 561 CTTCGGCGAA CCGCGCAGCG GCAATCAGGC CTTCGCGTCG TACATGAACG ATGCCTTCCA AGCCTCGAGC PDTT QYF RVT HAND GIP NLP PVE Q CCAGATACGA CGCAGTATTT CCGGGTCACT CATGCCAACG ACGGCATCCC AAACCTGCCC CCGGTGGAGC 631 NcoI ~~~~~ · G Y A H G G V E Y W S V D P Y S A Q N T F V C · 701 AGGGGTACGC CCATGGCGGT GTAGAGTACT GGAGCGTTGA TCCTTACAGC GCCCAGAACA CATTTGTCTG · T G D E V Q C C E A Q G G Q G V N N A H T T Y CACTGGGGAT GAAGTGCAGT GCTGTGAGGC CCAGGGCGGA CAGGGTGTGA ATAATGCGCA CACGACTTAT 771 SphI NotI FGMTSGACTWPVAAAEPLKDEL\* TTTGGGATGA CGAGCGGCG ATGCACCTGG CCGGTCGCGG CCGCGGAACC ACTGAAGGAT GAGCTGTAAA 841 GAAGCAGATC GTTCAAACAT TTGGCAATAA AGTTTCTTAA GATTGAATCC TGTTGCCGGT CTTGCGATGA 911 TTATCATATA ATTTCTGTTG AATTACGTTA AGCATGTAAT AATTAACATG TAATGCATGA CGTTATTTAT 981 GAGATGGGTT TTTATGATTA GAGTCCCGCA ATTATACATT TAATACGCGA TAGAAAACAA AATATAGCGC HindIII ClaI XbaI GCAAACTAGG ATAAATTATC GCGCGCGGTG TCATCTATGT TACTAGATCG ATAAGCTTCT AGAGCGGCCG 1121 GTGGAGCTCC AATTCGCCCT ATAGTGAGTC GTATTACGCG CGCTCACTGG CCGTCGTTTT ACAACGTCGT 1191 GACTGGGAAA ACCCTGGCGT TACCCAACTT AATCGCCTTG CAGCACATCC CCCTTTCGCC AGCTGGCGTA ATAGCGAAGA GGCCCGCACC GATCGCCCTT CCCAACAGTT GCGCAGCCTG AATGGCGAAT GGGACGCGCC 1331 CTGTAGCGGC GCATTAAGCG CGGCGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT TGCCAGCGCC 1401 CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG CCACGTTCGC CGGCTTTCCC CGTCAAGCTC 1471 TAAATCGGGG GCTCCCTTTA GGGTTCCGAT TTAGTGCTTT ACGGCACCTC GACCCCAAAA AACTTGATTA GGGTGATGGT TCACGTAGTG GGCCATCGCC CTGATAGACG GTTTTTCGCC CTTTGACGTT GGAGTCCACG TTCTTTAATA GTGGACTCTT GTTCCAAACT GGAACAACAC TCAACCCTAT CTCGGTCTAT TCTTTTGATT 1681

TATAAGGGAT TTTGCCGATT TCGGCCTATT GGTTAAAAAA TGAGCTGATT TAACAAAAAT TTAACGCGAA

# Fig. 47 C

|         | 1821 | TTTTAACAAA     | ATATTAACGC            | TTACAATTTA         | GGTGGCACTT | TTCGGGGAAA         | TGTGCGCGGA           | ACCCCTATTT         |
|---------|------|----------------|-----------------------|--------------------|------------|--------------------|----------------------|--------------------|
|         | 1891 |                |                       |                    | ATCCGCTCAT |                    |                      |                    |
|         | 1961 |                |                       | -                  | ACATTTCCGT |                    |                      |                    |
|         | 2031 |                |                       |                    | CTGGTGAAAG |                    |                      |                    |
|         | 2101 |                |                       |                    | GCGGTAAGAT |                    |                      |                    |
|         |      |                |                       |                    |            |                    |                      |                    |
|         | 2171 |                |                       |                    | ATGTGGCGCG |                    |                      |                    |
|         | 2241 |                |                       |                    | AATGACTTGG |                    |                      |                    |
|         | 2311 |                |                       |                    | GCAGTGCTGC |                    |                      |                    |
|         | 2381 |                |                       |                    | GGAGCTAACC |                    |                      |                    |
|         | 2451 |                |                       |                    | AATGAAGCCA |                    |                      |                    |
|         | 2521 |                |                       |                    | TATTAACTGG |                    |                      |                    |
|         | 2591 | ATTAATAGAC     | TGGATGGAGG            | CGGATAAAGT         | TGCAGGACCA | CTTCTGCGCT         | CGGCCCTTCC           | GGCTGGCTGG         |
|         | 2661 | TTTATTGCTG     | ATAAATCTGG            | AGCCGGTGAG         | CGTGGGTCTC | GCGGTATCAT         | TGCAGCACTG           | GGGCCAGATG         |
|         | 2731 | GTAAGCCCTC     | CCGTATCGTA            | GTTATCTACA         | CGACGGGGAG | TCAGGCAACT         | ATGGATGAAC           | GAAATAGACA         |
|         | 2801 |                |                       |                    | GCATTGGTAA |                    |                      |                    |
|         | 2871 | TAGATTGATT     | TAAAACTTCA            | ${\tt TTTTTAATTT}$ | AAAAGGATCT | AGGTGAAGAT         | CCTTTTTGAT           | AATCTCATGA         |
|         | 2941 | CCAAAATCCC     | TTAACGTGAG            | TTTTCGTTCC         | ACTGAGCGTC | AGACCCCGTA         | GAAAAGATCA           | AAGGATCTTC         |
|         | 3011 | TTGAGATCCT     | $\mathtt{TTTTTTCTGC}$ | GCGTAATCTG         | CTGCTTGCAA | ACAAAAAAAC         | CACCGCTACC           | AGCGGTGGTT         |
|         | 3081 | TGTTTGCCGG     | ATCAAGAGCT            | ACCAACTCTT         | TTTCCGAAGG | TAACTGGCTT         | CAGCAGAGCG           | CAGATACCAA         |
|         | 3151 | ATACTGTCCT     | TCTAGTGTAG            | CCGTAGTTAG         | GCCACCACTT | CAAGAACTCT         | GTAGCACCGC           | CTACATACCT         |
|         | 3221 | CGCTCTGCTA     | ATCCTGTTAC            | CAGTGGCTGC         | TGCCAGTGGC | GATAAGTCGT         | GTCTTACCGG           | GTTGGACTCA         |
|         | 3291 | AGACGATAGT     | TACCGGATAA            | GGCGCAGCGG         | TCGGGCTGAA | CGGGGGGTTC         | GTGCACACAG           | CCCAGCTTGG         |
| AC 2004 | 3361 | AGCGAACGAC     | CTACACCGAA            | CTGAGATACC         | TACAGCGTGA | GCTATGAGAA         | AGCGCCACGC           | TTCCCGAAGG         |
|         | 3431 | GAGAAAGGCG     | GACAGGTATC            | CGGTAAGCGG         | CAGGGTCGGA | ACAGGAGAGC         | GCACGAGGGA           | GCTTCCAGGG         |
|         | 3501 |                |                       |                    | GGGTTTCGCC |                    |                      |                    |
| 1. P 3  | 3571 |                |                       |                    | ACGCCAGCAA |                    |                      |                    |
| .Ci     | 3641 |                |                       |                    | GTTATCCCCT |                    |                      |                    |
|         | 3711 |                |                       |                    | ACGACCGAGC |                    |                      |                    |
| i.      | 3781 |                |                       |                    | CGCGTTGGCC |                    |                      |                    |
| Hand.   | 3851 |                |                       |                    | CGCAATTAAT |                    |                      |                    |
|         | 3921 |                |                       |                    | TTGTGTGGAA |                    |                      |                    |
|         | 3921 | GCITIACACI     | TIMIGCITCC            | GGC1CG1A1G         | AADDIDIDII | TIGIGAGCGG         | HIMACAMIII           | KpnI               |
|         |      |                |                       |                    |            |                    |                      | ~~                 |
| æ       | 3991 | A CAGCTATGA    | CCATCATTAC            | GCCN AGCGCG        | CAATTAACCC | TCACTAAACC         | CAACAAAACC           |                    |
|         | 329± | Xho            |                       | GCCAAGCGCG         | CAMITANCCC | ICACIAMIOO         | OMICAMANGC           | IGGGIACCGG         |
|         |      |                | ~~~                   |                    |            |                    |                      |                    |
|         | 4061 |                |                       | ለ ጥ ለ ጥር/ ርጥጥር ለ   | GAAGAGAGTC | ርርር እጥ አርጥርር       | אאמתתחאאאמי          | እ                  |
|         | 4131 |                |                       |                    | AAAGGTGGTA |                    |                      |                    |
|         | 4201 |                |                       |                    | TAAAAATTGA |                    |                      |                    |
|         | 4271 |                |                       |                    | GCGATTTGGA |                    |                      |                    |
| ļ.      | 4341 |                |                       |                    | TTGTATAAGA |                    |                      |                    |
| P-m:    | #3#T | AGIICGIIGC     | IIIIGIAAI             | ACAGAGGAI          | ECORI      | ARIAICIIIA         | AAAAACCCAI           | AIGCIAAIII         |
|         |      |                |                       |                    | ECORI      |                    |                      |                    |
|         | 4411 | ርኔ ርኔ ተኔ ኔ ተጥጥ | TTCDCDDDDD            | <b>ጥ</b> ልጥልጥልጥጥረግ | GGCGAATTCC | <u> አርያያ</u> ውርያያው | מיים א ליים א ליים א | ጥል ል ል ል ጥ አ ር ረ ጥ |
|         | 4481 |                |                       |                    | TAGTAAAATA |                    |                      |                    |
|         | 4551 |                |                       |                    | GTGCTATGCA |                    |                      |                    |
|         | 4621 |                |                       |                    | GGCAAATAGT |                    |                      |                    |
|         |      |                |                       |                    | AAAAAAAAAG |                    |                      |                    |
|         | 4691 |                |                       |                    |            |                    |                      |                    |
|         | 4761 |                |                       |                    | GAGGAGGATC |                    |                      |                    |
|         | 4831 |                |                       |                    | TATATACATA |                    |                      |                    |
|         | 4901 |                |                       |                    | CCTCGCTGCC |                    |                      |                    |
|         | 4971 |                |                       |                    | CTCTTTCTTT |                    |                      |                    |
|         | 5041 | CTTTGGCCTT     | GGTAGTTTGG            | GTGGGCGAGA         | GCGGCTTCGT | CGCCCAGATC         | GGTGCGCGGG           |                    |
|         |      |                |                       |                    | BamHI      |                    |                      | BglII              |
|         |      |                |                       |                    | ~~~~       |                    |                      |                    |
|         | 5111 |                | GGCGTCTCCG            | GGCGTGAGTC         | GGCCCGGATC | CTCGCGGGGA         | ATGGGGCTCT           | CGGATGTAGA         |
|         |      | BglII          |                       |                    |            |                    |                      |                    |
|         |      | ~~~            |                       |                    | _          |                    |                      |                    |
|         | 5181 |                |                       |                    | TTTGAATCCC |                    | TCATCGGTAG           | TTTTTCTTTT         |
|         |      |                |                       |                    |            |                    |                      |                    |
|         | 5251 | CATGATTTGT     | GACAAATGCA            | GCCTCGTGCG         | GAGCTTTTTT | GTAGC              |                      |                    |



### Sequence for pUB8.11

NcoI

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KpnI

1 CATGGGCCAG GTATAATTAT GGGATATCTC AAGCAAATAA TCGAAATATC ACCATTGGCT ACAATATCTG

GTACCCGGTC CATATTAATA CCCTATAGAG TTCGTTTATT AGCTTTATAG TGGTAACCGA TGTTATAGAC

PstI XbaI XbaI

~~~~~

71 AGCTCCGAGT TCTGACTGCA GTCTGGATGA CGCGTGTTGT ATCTAGAACT CTAGATAGCA CAGCCACAGC

TCGAGGCTCA AGACTGACGT CAGACCTACT GCGCACAACA TAGATCTTGA GATCTATCGT GTCGGTGTCG

141 ACCTACAGGA GTGCGACACT TGTGGACTGT AGTAGTGTTG GAGACGGAGC TCTTTCCTAC CTCCTGACGT

TGGATGTCCT CACGCTGTGA ACACCTGACA TCATCACAAC CTCTGCCTCG AGAAAGGATG GAGGACTGCA

211 TGCCGCCGTT GTCCATTCCA ACGGCATCAC TCTCAACCAA TCACGCGCTC CCAACAAAAT ATCGTCCCCC

 ${\tt ACGGCGGCAA} \ \ {\tt CAGGTAAGGT} \ \ {\tt TGCCGTAGTG} \ \ {\tt AGAGTTGGTT} \ \ {\tt AGTGCGCGAG}$   ${\tt GGTTGTTTA} \ \ {\tt TAGCAGGGGG}$ 

281 ATGTCTTGGC GGAGAGAGA TACATACATG CTGTCGCGCC GTTTTTGTCT GAATCTCGCT TCCACTGGCC

TACAGAACCG CCTCTCTCTC ATGTATGTAC GACAGCGCGG CAAAAACAGA

### SmaI

351 AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA

TTAGTCGAGT CGAGGGCCCT CGAGTGAGTA AGTTCTAGGG TAGCAGCAGC AGTGGGGACC GCAGTACCCT

421 TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT

ACCTTTCTT GGAGGCAACG AGCCTACTCA GTCGGTATAG GGGCTTGTCT

### SphI

~~~~~

491 TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG

AGTCTAAGGG GGTTATCTCT TTCATATCGT ACGAAAGCCC AAAACAAACC GAATTAACTG AAATAAAAAC

561 TTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG

AACCTCAACT TACGACTAAA CAACACATTT TACGGGTTGG TAGACTTATA GCTCTGCCTA TTATCCGACC

631 CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT

GATTAATTAA ATATCGTTCT AAGACATCAC GTGTAGCGTT TATAGAAAGA CCCGTAATGT CGACCTCCGA

#### PstI

701 TCATCAGCCT GAAACACTCT GCAGAGCCTG AAGCAAGTGG TGAAGCGTGG CGATGAGATG GGTATAAAAC

AGTAGTCGGA CTTTGTGAGA CGTCTCGGAC TTCGTTCACC ACTTCGCACC GCTACTCTAC CCATATTTTG

TCCCCCTGCC GGACGACCCA

AGGGGGACGG CCTGCTGGGT

841 GTAAAATACT GTTGCCCACT CGCCGGCGAG ATGGCCCACG GCCGCATCCT CTTCTTGGCG CTCGCCGTCT

CATTTTATGA CAACGGGTGA GCGGCCGCTC TACCGGGTGC CGGCGTAGGA GAAGAACCGC GAGCGGCAGA

BssHII

~~~~~

NotI

911 TGGCCACCGC CGCGGTGGCC GCCGCATCNT TGGCGGACTC CAACCCGATC CGGCCCGTCA CCGAGCGCGC

ACCGGTGGCG GCGCCACCGG CGGCGTAGNA ACCGCCTGAG GTTGGGCTAG GCCGGGCAGT GGCTCGCGCG

NotI

981 GGCCGCCTCC ACGCAGGGCA TCTCCGAAGA CCTCTACAGC CGTTTAGTCG AAATGGCCAC TATCTCCCAA

CCGGCGGAGG TGCGTCCCGT AGAGGCTTCT GGAGATGTCG GCAAATCAGC TTTACCGGTG ATAGAGGGTT

> SalI ~~~~~

> > AccI

1051 GCTGCCTACG CCGACCTGTG CAACATTCCG TCGACTATTA TCAAGGGAGA GAAAATTTAC AATTCTCAAA

Fig. 48 C

CGACGGATGC GGCTGGACAC GTTGTAAGGC AGCTGATAAT AGTTCCCTCT

#### BamHI

~~~~~

1121 CTGACATTAA CGGATGGATC CTCCGCGACG ACAGCAGCAA AGAAATAATC ACCGTCTTCC GTGGCACTGG

GACTGTAATT GCCTACCTAG GAGGCGCTGC TGTCGTCGTT TCTTTATTAG
TGGCAGAAGG CACCGTGACC

1191 TAGTGATACG AATCTACAAC TCGATACTAA CTACACCCTC ACGCCTTTCG ACACCCTACC ACAATGCAAC

ATCACTATGC TTAGATGTTG AGCTATGATT GATGTGGGAG TGCGGAAAGC TGTGGGATGG TGTTACGTTG

1261 GGTTGTGAAG TACACGGTGG ATATTATATT GGATGGGTCT CCGTCCAGGA CCAAGTCGAG TCGCTTGTCA

CCAACACTTC ATGTGCCACC TATAATATAA CCTACCCAGA GGCAGGTCCT GGTTCAGCTC AGCGAACAGT

1331 AACAGCAGGT TAGCCAGTAT CCGGACTACG CGCTGACCGT GACCGGCCAC KCCCTCGGCG CCTCCCTGGC

TTGTCGTCCA ATCGGTCATA GGCCTGATGC GCGACTGGCA CTGGCCGGTG MGGGAGCCGC GGAGGGACCG

1401 GGCACTCACT GCCGCCCAGC TGTCTGCGAC ATACGACAAC ATCCGCCTGT ACACCTTCGG CGAACCGCGC

CCGTGAGTGA CGGCGGGTCG ACAGACGCTG TATGCTGTTG TAGGCGGACA TGTGGAAGCC GCTTGGCGCG

XhoI

~~~~~

1471 AGCGGCAATC AGGCCTTCGC GTCGTACATG AACGATGCCT TCCAAGCCTC GAGCCCAGAT ACGACGCAGT

NcoI

~~~~

1541 ATTTCCGGGT CACTCATGCC AACGACGGCA TCCCAAACCT GCCCCCGGTG GAGCAGGGGT ACGCCCATGG

TAAAGGCCCA GTGAGTACGG TTGCTGCCGT AGGGTTTGGA CGGGGGCCAC CTCGTCCCCA TGCGGGTACC

1611 CGGTGTAGAG TACTGGAGCG TTGATCCTTA CAGCGCCCAG AACACATTTG TCTGCACTGG GGATGAAGTG

GCCACATCTC ATGACCTCGC AACTAGGAAT GTCGCGGGTC TTGTGTAAAC AGACGTGACC CCTACTTCAC

1681 CAGTGCTGTG AGGCCCAGGG CGGACAGGGT GTGAATAATG CGCACACGAC TTATTTTGGG ATGACGAGCG

GTCACGACAC TCCGGGTCCC GCCTGTCCCA CACTTATTAC GCGTGTGCTG
AATAAAACCC TACTGCTCGC

1751 GAGCCTGTAC ATGGTGATCA GTCATTTCAG CCTCCCCGAG TGTACCAGGA AAGATGGATG TCCTGGAGAG

CTCGGACATG TACCACTAGT CAGTAAAGTC GGAGGGGCTC ACATGGTCCT

1821 GGGGCCGCGT AACCACTGAA GGATGAGCTG TAAAGAAGCA GATCGTTCAA ACATTTGGCA ATAAAGTTTC

CCCCGGCGCA TTGGTGACTT CCTACTCGAC ATTTCTTCGT CTAGCAAGTT TGTAAACCGT TATTTCAAAG

1891 TTAAGATTGA ATCCTGTTGC CGGTCTTGCG ATGATTATCA TATAATTTCT GTTGAATTAC GTTAAGCATG

AATTCTAACT TAGGACAACG GCCAGAACGC TACTAATAGT ATATTAAAGA CAACTTAATG CAATTCGTAC

1961 TAATAATTAA CATGTAATGC ATGACGTTAT TTATGAGATG GGTTTTTATG ATTAGAGTCC CGCAATTATA

ATTATTAATT GTACATTACG TACTGCAATA AATACTCTAC CCAAAAATAC TAATCTCAGG GCGTTAATAT

BssHII

BssHII

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2031 CATTTAATAC GCGATAGAAA ACAAAATATA GCGCGCAAAC TAGGATAAAT
TATCGCGCGC GGTGTCATCT

GTAAATTATG CGCTATCTTT TGTTTTATAT CGCGCGTTTG ATCCTATTTA ATAGCGCGCG CCACAGTAGA

XbaI

~~~~~

### ClaI HindIII

2101 ATGTTACTAG ATCGATAAGC TTCTAGAGCG GCCGGTGGAG CTCCAATTCG

CCCTATAGTG AGTCGTATTA

TACAATGATC TAGCTATTCG AAGATCTCGC CGGCCACCTC GAGGTTAAGC GGGATATCAC TCAGCATAAT

BssHII

~~~~

2171 CGCGCGCTCA CTGGCCGTCG TTTTACAACG TCGTGACTGG GAAAACCCTG

GCGCGCGAGT GACCGGCAGC AAAATGTTGC AGCACTGACC CTTTTGGGAC CGCAATGGGT TGAATTAGCG

2241 CTTGCAGCAC ATCCCCCTTT CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC

GAACGTCGTG TAGGGGGAAA GCGGTCGACC GCATTATCGC TTCTCCGGGC GTGGCTAGCG GGAAGGGTTG

Fig. 48 E

2311 AGTTGCGCAG CCTGAATGGC GAATGGGACG CGCCCTGTAG CGGCGCATTA AGCGCGGCGG GTGTGGTGGT

TCAACGCGTC GGACTTACCG CTTACCCTGC GCGGGACATC GCCGCGTAAT TCGCGCCGCC CACACCACCA

2381 TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT CCCTTCCTTT

ATGCGCGTCG CACTGGCGAT GTGAACGGTC GCGGGATCGC GGGCGAGGAA AGCGAAAGAA GGGAAGGAAA

2451 CTCGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAAATC GGGGGCTCCC
TTTAGGGTTC CGATTTAGTG

GAGCGGTGCA AGCGGCCGAA AGGGGCAGTT CGAGATTTAG CCCCCGAGGG AAATCCCAAG GCTAAATCAC

 $2521\,$  CTTTACGGCA CCTCGACCCC AAAAAACTTG ATTAGGGTGA TGGTTCACGT AGTGGGCCAT CGCCCTGATA

GAAATGCCGT GGAGCTGGGG TTTTTTGAAC TAATCCCACT ACCAAGTGCA TCACCCGGTA GCGGGACTAT

2591 GACGGTTTTT CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCTTGTTCCA AACTGGAACA

CTGCCAAAAA GCGGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACCTG

2661 ACACTCAACC CTATCTCGGT CTATTCTTTT GATTTATAAG GGATTTTGCC GATTTCGGCC TATTGGTTAA

TGTGAGTTGG GATAGAGCCA GATAAGAAAA CTAAATATTC CCTAAAACGG CTAAAGCCGG ATAACCAATT

2731 AAAATGAGCT GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA ACGCTTACAA TTTAGGTGGC

TTTTACTCGA CTAAATTGTT TTTAAATTGC GCTTAAAATT GTTTTATAAT TGCGAATGTT AAATCCACCG

2801 ACTTTTCGGG GAAATGTGCG CGGAACCCCT ATTTGTTTAT TTTTCTAAAT ACATTCAAAT ATGTATCCGC

TGAAAAGCCC CTTTACACGC GCCTTGGGGA TAAACAAATA AAAAGATTTA TGTAAGTTTA TACATAGGCG

2871 TCATGAGACA ATAACCCTGA TAAATGCTTC AATAATATTG AAAAAGGAAG AGTATGAGTA TTCAACATTT

AGTACTCTGT TATTGGGACT ATTTACGAAG TTATTATAAC TTTTTCCTTC TCATACTCAT AAGTTGTAAA

2941 CCGTGTCGCC CTTATTCCCT TTTTTGCGGC ATTTTGCCTT CCTGTTTTTG

GGCACAGCGG GAATAAGGGA AAAAACGCCG TAAAACGGAA GGACAAAAACGGGGTCT TTGCGACCAC

3011 AAAGTAAAAG ATGCTGAAGA TCAGTTGGGT GCACGAGTGG GTTACATCGA ACTGGATCTC AACAGCGGTA

TTTCATTTTC TACGACTTCT AGTCAACCCA CGTGCTCACC CAATGTAGCT TGACCTAGAG TTGTCGCCAT

- $3\,08\,1$  AGATCCTTGA GAGTTTTCGC CCCGAAGAAC GTTTTCCAAT GATGAGCACT TTTAAAGTTC TGCTATGTGG
- TCTAGGAACT CTCAAAAGCG GGGCTTCTTG CAAAAGGTTA CTACTCGTGA AAATTTCAAG ACGATACACC
- 3151 CGCGGTATTA TCCCGTATTG ACGCCGGGCA AGAGCAACTC GGTCGCCGCA TACACTATTC TCAGAATGAC
- GCGCCATAAT AGGGCATAAC TGCGGCCCGT TCTCGTTGAG CCAGCGGCGT ATGTGATAAG AGTCTTACTG
- 3221 TTGGTTGAGT ACTCACCAGT CACAGAAAAG CATCTTACGG ATGGCATGAC AGTAAGAGAA TTATGCAGTG
- AACCAACTCA TGAGTGGTCA GTGTCTTTTC GTAGAATGCC TACCGTACTG
- 3291 CTGCCATAAC CATGAGTGAT AACACTGCGG CCAACTTACT TCTGACAACG ATCGGAGGAC CGAAGGAGCT
- GACGGTATTG GTACTCACTA TTGTGACGCC GGTTGAATGA AGACTGTTGC TAGCCTCCTG GCTTCCTCGA
- 3361 AACCGCTTTT TTGCACAACA TGGGGGATCA TGTAACTCGC CTTGATCGTT GGGAACCGGA GCTGAATGAA
- TTGGCGAAAA AACGTGTTGT ACCCCCTAGT ACATTGAGCG GAACTAGCAA
- 3431 GCCATACCAA ACGACGAGCG TGACACCACG ATGCCTGTAG CAATGGCAAC AACGTTGCGC AAACTATTAA
- CGGTATGGTT TGCTGCTCGC ACTGTGGTGC TACGGACATC GTTACCGTTG
  TTGCAACGCG TTTGATAATT
- 3501 CTGGCGAACT ACTTACTCTA GCTTCCCGGC AACAATTAAT AGACTGGATG GAGGCGGATA AAGTTGCAGG
- GACCGCTTGA TGAATGAGAT CGAAGGGCCG TTGTTAATTA TCTGACCTAC CTCCGCCTAT TTCAACGTCC
- 3571 ACCACTTCTG CGCTCGGCCC TTCCGGCTGG CTGGTTTATT GCTGATAAAT
- TGGTGAAGAC GCGAGCCGGG AAGGCCGACC GACCAAATAA CGACTATTTA
- 3641 TCTCGCGGTA TCATTGCAGC ACTGGGGCCA GATGGTAAGC CCTCCCGTAT
- AGAGCGCCAT AGTAACGTCG TGACCCCGGT CTACCATTCG GGAGGGCATA GCATCAATAG ATGTGCTGCC
- 3711 GGAGTCAGGC AACTATGGAT GAACGAAATA GACAGATCGC TGAGATAGGT GCCTCACTGA TTAAGCATTG
- CCTCAGTCCG TTGATACCTA CTTGCTTTAT CTGTCTAGCG ACTCTATCCA CGGAGTGACT AATTCGTAAC
- 3781 GTAACTGTCA GACCAAGTTT ACTCATATAT ACTTTAGATT GATTTAAAACC TTCATTTTTA ATTTAAAAGG

CATTGACAGT CTGGTTCAAA TGAGTATATA TGAAATCTAA CTAAATTTTG AAGTAAAAAT TAAATTTTCC

3851 ATCTAGGTGA AGATCCTTTT TGATAATCTC ATGACCAAAA TCCCTTAACG TGAGTTTTCG TTCCACTGAG

TAGATCCACT TCTAGGAAAA ACTATTAGAG TACTGGTTTT AGGGAATTGC ACTCAAAAGC AAGGTGACTC

3921 CGTCAGACCC CGTAGAAAAG ATCAAAGGAT CTTCTTGAGA TCCTTTTTTT CTGCGCGTAA TCTGCTGCTT

GCAGTCTGGG GCATCTTTTC TAGTTTCCTA GAAGAACTCT AGGAAAAAAA GACGCGCATT AGACGACGAA

3991 GCAAACAAA AAACCACCGC TACCAGCGGT GGTTTGTTTG CCGGATCAAG AGCTACCAAC TCTTTTTCCG

CGTTTGTTTT TTTGGTGGCG ATGGTCGCCA CCAAACAAAC GGCCTAGTTC TCGATGGTTG AGAAAAAGGC

4061 AAGGTAACTG GCTTCAGCAG AGCGCAGATA CCAAATACTG TCCTTCTAGT GTAGCCGTAG TTAGGCCACC

TTCCATTGAC CGAAGTCGTC TCGCGTCTAT GGTTTATGAC AGGAAGATCA CATCGGCATC AATCCGGTGG

4131 ACTTCAAGAA CTCTGTAGCA CCGCCTACAT ACCTCGCTCT GCTAATCCTG TTACCAGTGG CTGCTGCCAG

TGAAGTTCTT GAGACATCGT GGCGGATGTA TGGAGCGAGA CGATTAGGAC AATGGTCACC GACGACGGTC

4201 TGGCGATAAG TCGTGTCTTA CCGGGTTGGA CTCAAGACGA TAGTTACCGG ATAAGGCGCA GCGGTCGGGC

ACCGCTATTC AGCACAGAAT GGCCCAACCT GAGTTCTGCT ATCAATGGCC

4271 TGAACGGGGG GTTCGTGCAC ACAGCCCAGC TTGGAGCGAA CGACCTACAC CGAACTGAGA TACCTACAGC

ACTTGCCCCC CAAGCACGTG TGTCGGGTCG AACCTCGCTT GCTGGATGTG

4341 GTGAGCTATG AGAAAGCGCC ACGCTTCCCG AAGGGAGAAA GGCGGACAGG
TATCCGGTAA GCGGCAGGGT

CACTCGATAC TCTTTCGCGG TGCGAAGGGC TTCCCTCTTT CCGCCTGTCC ATAGGCCATT CGCCGTCCCA

4411 CGGAACAGGA GAGCGCACGA GGGAGCTTCC AGGGGGAAAC GCCTGGTATC

GCCTTGTCCT CTCGCGTGCT CCCTCGAAGG TCCCCCTTTG CGGACCATAG

GCGGTGGAGA CTGAACTCGC AGCTAAAAAC ACTACGAGCA GTCCCCCCGC CTCGGATACC TTTTTGCGGT

4551 GCAACGCGGC CTTTTTACGG TTCCTGGCCT TTTGCTGGCC TTTTGCTCAC ATGTTCTTTC CTGCGTTATC

CGTTGCGCCG GAAAAATGCC AAGGACCGGA AAACGACCGG AAAACGAGTG

4621 CCCTGATTCT GTGGATAACC GTATTACCGC CTTTGAGTGA GCTGATACCG CTCGCCGCAG CCGAACGACC

GGGACTAAGA CACCTATTGG CATAATGGCG GAAACTCACT CGACTATGGC GAGCGGCGTC GGCTTGCTGG

4691 GAGCGCAGCG AGTCAGTGAG CGAGGAAGCG GAAGAGCGCC CAATACGCAA ACCGCCTCTC CCCGCGCGTT

CTCGCGTCGC TCAGTCACTC GCTCCTTCGC CTTCTCGCGG GTTATGCGTT

4761 GGCCGATTCA TTAATGCAGC TGGCACGACA GGTTTCCCGA CTGGAAAGCG GGCAGTGAGC GCAACGCAAT

CCGGCTAAGT AATTACGTCG ACCGTGCTGT CCAAAGGGCT GACCTTTCGC CCGTCACTCG CGTTGCGTTA

4831 TAATGTGAGT TAGCTCACTC ATTAGGCACC CCAGGCTTTA CACTTTATGC TTCCGGCTCG TATGTTGTGT

ATTACACTCA ATCGAGTGAG TAATCCGTGG GGTCCGAAAT GTGAAATACG

BssHII

~~~~~

4901 GGAATTGTGA GCGGATAACA ATTTCACACA GGAAACAGCT ATGACCATGA

TTACGCCAAG CGCGCAATTA

CCTTAACACT CGCCTATTGT TAAAGTGTGT CCTTTGTCGA TACTGGTACT AATGCGGTTC GCGCGTTAAT

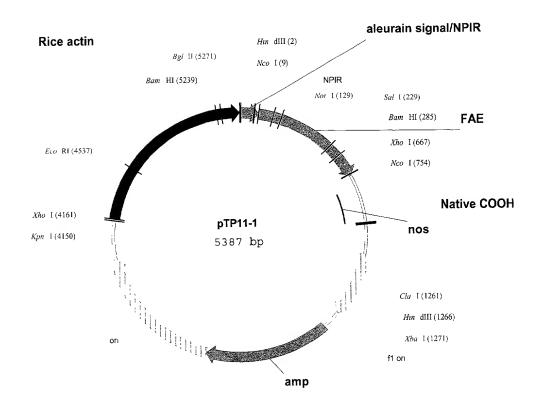
NcoI

KpnI

~~~

4971 ACCCTCACTA AAGGGAACAA AAGCTGGGTA C TGGGAGTGAT TTCCCTTGTT TTCGACCCAT G

# Figure 49 A



281

351

### Figure 49B

NcoI

| TT   | - J T       | TT      |
|------|-------------|---------|
| HII. | $_{\rm LL}$ | . 1. 1. |

M A H A R V L L L A L A V L A T A A V A V

1 AAGCTTACCA TGGCCCACGC CCGCGTCCTC CTCCTGGCGC TCGCCGTGCT GGCCACGGCC GCCGTCGCCG

Noti

. A S S S S F A D S N P I R P V T D R A A A S T .

TCGCCTCCTC CTCCTCCTTC GCCGACTCCA ACCCGATCCG GCCCGTCACC GACCGCGCGG CCGCCTCCAC

Q G I S E D L Y S R L V E M A T I S Q A A Y A

GCAGGGCATC TCCGAAGACC TCTACAGCCG TTTAGTCGAA ATGGCCACTA TCTCCCAAGC TGCCTACGCC

### SalI ~~~~~

### AccI

D L C N I P S T I I K G E K I Y N S Q T D I N G ACCTGTGCA ACATTCCGTC GACTATTATC AAGGGAGAGA AAATTTACAA TTCTCAAACT GACATTAACG BAMHI

. W I L R D D S S K E I I T V F R G T G S D T N GATGGATCCT CCGCGACGAC AGCAGCAAAG AAATAATCAC CGTCTTCCGT GGCACTGGTA GTGATACGAA L Q L D T N Y T L T P F D T L P Q C N G C E V TCTACAACTC GATACTAACT ACACCCTCAC GCCTTTCGAC ACCCTACCAC AATGCAACGG TTGTGAAGTA H G G Y Y I G W V S V Q D Q V E S L V K Q Q V S CACGGTGGAT ATTATATTGG ATGGGTCTCC GTCCAGGACC AAGTCGAGTC GCTTGTCAAA CAGCAGGTTA Q Y P D Y A L T V T G H X L G A S L A A L T A GCCAGTATCC GGACTACGC CTGACCGTGA CCGGCCACKC CCTCGGCGC TCCCTGGCGG CACTCACTGC A Q L S A T Y D N I R L Y T F G E P R S G N Q CGCCCAGCTG TCTGCGACCAT ACGACAACAT CCGCCTGTAC ACCTTCGGCG AACCGCGCAG CGGCAATCAG XhoI

A F A S Y M N D A F Q A S S P D T T Q Y F R V T GCTTCGCGT CGTACATGAA CGATGCCTTC CAAGCCTCGA GCCCAGATAC GACGCAGTAT TTCCGGGTCA Ncol

. HANDGIPNLPPVE QGYAHGG VEY. CTCATGCCAA CGACGGCATC CCAAACCTGC CCCCGGTGGA GCAGGGGTAC GCCCATGGCG GTGTAGAGTA 701 . W S V D P Y S A Q N T F V C T G D E V Q C C E CTGGAGCGTT GATCCTTACA GCGCCCAGAA CACATTTGTC TGCACTGGGG ATGAAGTGCA GTGCTGTGAG 771 AQGGQGVNNA HTTY FGM TSG ACTW GCCCAGGGCG GACAGGGTGT GAATAATGCG CACACGACTT ATTTTGGGAT GACGAGCGGA GCCTGTACAT 841 GGTGATCAGT CATTTCAGCC TCCCCGAGTG TACCAGGAAA GATGGATGTC CTGGAGAGGG GGCCGCGTAA 911 CCACTGAAGG ATGAGCTGTA AAGAAGCAGA TCGTTCAAAC ATTTGGCAAT AAAGTTTCTT AAGATTGAAT CCTGTTGCCG GTCTTGCGAT GATTATCATA TAATTTCTGT TGAATTACGT TAAGCATGTA ATAATTAACA 1051 TGTAATGCAT GACGTTATTT ATGAGATGGG TTTTTATGAT TAGAGTCCCG CAATTATACA TTTAATACGC 1121

1191 GATAGAAAC AAAATATAGC GCGCAAACTA GGATAAATTA TCGCGCGCGG TGTCATCTAT GTTACTAGAT HindIII

### ClaI XbaI

CGATAAGCTT CTAGAGCGGC CGGTGGAGCT CCAATTCGCC CTATAGTGAG TCGTATTACG CGCGCTCACT

1331 GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC TTAATCGCCT TGCAGCACAT

1401 CCCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATCGCC TTCCCAACAG TTGCCGCAGCC

1471 TGAATGGCGA ATGGGACGCG CCCTGTAGCG GCGCATTAAG CGCGGCGGGT GTGGTGGTTA CGCCAGCGT

1541 GACCGCTACA CTTGCCAGCG CCCTAGCGC CGCTCCTTTC GCTTCTTCC CTCCTTTCT CGCCACGTT

1611 GCCGGCTTC CCCGTCAAGC TCTAAATCGG GGGCTCCCTT TAGGGTTCCG ATTTAGTGCT TTACGGCACC

1681 TCGACCCCAA AAAACTTGAT TAGGGTGATG GTTCACGTAG TGGGCCATCG CCCTGATAGA CGGTTTTCCC

# Fig. 49 C

|                                        |                                                                              |                                                   |                                              |                        | •                                      |                             |             |                          |  |  |
|----------------------------------------|------------------------------------------------------------------------------|---------------------------------------------------|----------------------------------------------|------------------------|----------------------------------------|-----------------------------|-------------|--------------------------|--|--|
|                                        | 1751                                                                         | CCCTTTGACG                                        | TTGGAGTCCA                                   | CGTTCTTTAA             | TAGTGGACTC                             | TTGTTCCAAA                  | CTGGAACAAC  | ACTCAACCCT               |  |  |
|                                        | 1821                                                                         | $\lambda$ TOTOCOTOT                               | ᡘ᠇ᡎᠬᡎᡎᡎ᠘᠘                                    | TTTATAAGGG             | ATTTTGCCGA                             | TTTCGGCCTA                  | TTGGTTAAAA  | AATGAGCTGA               |  |  |
|                                        | 1891                                                                         | ጥጥጥአ አ ር' አ ል ል ል                                 | ATTTA ACGCG                                  | AATTTTAACA             | AAATATTAAC                             | GCTTACAATT                  | TAGGTGGCAC  | TTTTCGGGGA               |  |  |
|                                        | 1961                                                                         | $\lambda$ $\lambda$ TCTCCCCC                      | CAACCCCTAT                                   | TTGTTTATTT             | TTCTAAATAC                             | ATTCAAATAT                  | GTATCCGCTC  | ATGAGACAAT               |  |  |
|                                        | 2031                                                                         | A A CCCTGATA                                      | AATGCTTCAA                                   | TAATATTGAA             | AAAGGAAGAG                             | TATGAGTATT                  | CAACATTTCC  | GIGICGCCCI               |  |  |
|                                        | 2101                                                                         | ᅲᄼᇄᆄᄼᄼᄼᅼᆔᅲᅲ                                       | TATTCCCCCAT                                  | TTTGCCTTCC             | TGTTTTTGCT                             | CACCCAGAAA                  | CGCTGGTGAA  | AGTAAAAGAT               |  |  |
|                                        | 2171                                                                         | CCTCAACATC                                        | ∆GTTGGGTGC                                   | ACGAGTGGGT             | TACATCGAAC                             | TGGATCTCAA                  | CAGCGGTAAG  | ATCCTTGAGA               |  |  |
|                                        | 2241                                                                         | CTTTTTTCCCCC                                      | CGAAGAACGT                                   | TTTCCAATGA             | TGAGCACTTT                             | TAAAGTTCTG                  | CTATGTGGCG  | CGGTATTATC               |  |  |
|                                        | 2311                                                                         | CCCTDTTCDC                                        | GCCGGGCAAG                                   | AGCAACTCGG             | TCGCCGCATA                             | CACTATTCTC                  | AGAATGACTT  | GGTTGAGTAC               |  |  |
|                                        | 2381                                                                         | TCDCCDCTCD                                        | CAGAAAAGCA                                   | TCTTACGGAT             | GGCATGACAG                             | TAAGAGAATT                  | ATGCAGTGCT  | GCCATAACCA               |  |  |
|                                        | 2451                                                                         | ጥር እርጥር ልጥል ል                                     | CACTGCGGCC                                   | AACTTACTTC             | TGACAACGAT                             | CGGAGGACCG                  | AAGGAGCTAA  | CCGCTTTTTT               |  |  |
|                                        | 2521                                                                         | CCACAACATC                                        | CCCCATCATC                                   | $T\Delta\DeltaCTCGCCT$ | TGATCGTTGG                             | GAACCGGAGC                  | TGAATGAAGC  | CATACCAAAC               |  |  |
|                                        | 2591                                                                         | CACCACCGTC                                        | ACACCACGAT                                   | GCCTGTAGCA             | ATGGCAACAA                             | CGTTGCGCAA                  | ACTATTAACT  | GGCGAACTAC               |  |  |
|                                        | 2661                                                                         | መመን የምርጥን ርር                                      | $TTCCCCCCC\Delta\Delta$                      | CAATTAATAG             | ACTGGATGGA                             | GGCGGATAAA                  | GTTGCAGGAC  | CACTTCTGCG               |  |  |
|                                        | 2731                                                                         | CTCCCCCCTT                                        | CCGCCTGGCT                                   | GGTTTATTGC             | TGATAAATCT                             | GGAGCCGGTG                  | AGCGTGGGTC  | TCGCGGTATC               |  |  |
|                                        | 2801                                                                         | አ ምጥርር አርር <mark>አ</mark> ር                       | TCCCCCCAGA                                   | TGGTAAGCCC             | TCCCGTATCG                             | TAGTTATCTA                  | CACGACGGGG  | AGTCAGGCAA               |  |  |
|                                        | 2871                                                                         | CTATCCATCA                                        | ACGAAATAGA                                   | CAGATCGCTG             | AGATAGGTGC                             | CTCACTGATT                  | AAGCATTGGT  | AACTGTCAGA               |  |  |
|                                        | 2941                                                                         | CCXXCTTTXC                                        | $TC\Delta T\Delta T\Delta T\Delta T\Delta C$ | TTTAGATTGA             | TTTAAAACTT                             | CATTTTTAAT                  | TTAAAAGGAT  | CTAGGTGAAG               |  |  |
|                                        | 3011                                                                         | $^{2}$                                            | ለጥ <u>ለ</u> ልጥርጥርልጥ                          | CACCAAAATC             | CCTTAACGTG                             | AGTTTTCGTT                  | CCACTGAGCG  | TCAGACCCCG               |  |  |
|                                        | 3081                                                                         | <b>ጥ</b> ክሮአአአአርልጥ                                | CAAACCATCT                                   | TCTTGAGATC             | CTTTTTTTCT                             | GCGCGTAATC                  | TGCTGCTTGC  | AAACAAAAAA               |  |  |
|                                        | 3151                                                                         | አ                                                 | CCAGCGGTGG                                   | TTTGTTTGCC             | GGATCAAGAG                             | CTACCAACTC                  | TTTTTCCGAA  | GGTAACTGGC               |  |  |
|                                        | 3221                                                                         | TTCACCACAC                                        | CGCAGATACC                                   | AAATACTGTC             | CTTCTAGTGT                             | AGCCGTAGTT                  | AGGCCACCAC  | TTCAAGAACT               |  |  |
|                                        | 3291                                                                         | ርጥርጥ አርር አርር                                      | GCCTACATAC                                   | CTCGCTCTGC             | TAATCCTGTT                             | ACCAGTGGCT                  | GCTGCCAGTG  | GCGATAAGTC               |  |  |
|                                        | 3361                                                                         | CTCTCTTACC                                        | CCCTTCCACT                                   | CAAGACGATA             | GTTACCGGAT                             | AAGGCGCAGC                  | GGTCGGGCTG  | AACGGGGGT                |  |  |
|                                        | 3431                                                                         | TOOTOONONC                                        | ACCCCACCTT                                   | GGAGCGAACG             | ACCTACACCG                             | AACTGAGATA                  | CCTACAGCGT  | GAGCTATGAG               |  |  |
|                                        | 3501                                                                         | $\lambda$ $\lambda$ $\lambda$ $C$ $C$ $C$ $C$ $C$ | CCTTCCCGAA                                   | GGGAGAAAGG             | CGGACAGGTA                             | TCCGGTAAGC                  | GGCAGGGTCG  | GAACAGGAGA               |  |  |
|                                        | 3571                                                                         | CCCCACGACG                                        | GAGCTTCCAG                                   | GGGGAAACGC             | CTGGTATCTT                             | TATAGTCCTG                  | TCGGGTTTCG  | CCACCTCTGA               |  |  |
|                                        | 3641                                                                         | CTTGACCGTC                                        | GATTTTTGTG                                   | ATGCTCGTCA             | GGGGGGCGGA                             | GCCTATGGAA                  | AAACGCCAGC  | AACGCGGCCT               |  |  |
|                                        | 3711                                                                         | መመመመን ሮርርጥጥ                                       | CCTCCCCTTT                                   | TGCTGGCCTT             | TTGCTCACAT                             | GTTCTTTCCT                  | GCGTTATCCC  | CTGAT TCTGT              |  |  |
|                                        | 3781                                                                         | CCATAACCCT                                        | $\Delta$ TT $\Delta$ CCGCCT                  | TTGAGTGAGC             | TGATACCGCT                             | CGCCGCAGCC                  | GAACGACCGA  | GCGCAGCGAG               |  |  |
| TU.                                    | 3851                                                                         | TCACTGAGCG                                        | AGGAAGCGGA                                   | AGAGCGCCCA             | ATACGCAAAC                             | CGCCTCTCCC                  | CGCGCGTTGG  | CCGATTCATT               |  |  |
|                                        | 3921                                                                         | $\lambda$ $\lambda$ $T$ CC $\lambda$ CCTC         | GCACGACAGG                                   | TTTCCCGACT             | ' GGAAAGCGGG                           | CAGTGAGCGC                  | AACGCAATTA  | ATGTGAGTTA               |  |  |
| 200                                    | 3991                                                                         | GCTCACTCAT                                        | TAGGCACCCC                                   | AGGCTTTACA             | . CTTTATGCTT                           | CCGGCTCGTA                  | TGTTGTGTGG  | AATTGTGAGC               |  |  |
| 11                                     | 4061                                                                         | GGATAACAAT                                        | TTCACACAGG                                   | AAACAGCTAT             | GACCATGATT                             | ACGCCAAGCG                  | CGCAATTAAC  | CCTCACTAAA               |  |  |
| ************************************** |                                                                              |                                                   | KpnI                                         |                        | XhoI                                   |                             |             |                          |  |  |
| i.a                                    |                                                                              |                                                   | ~~~~~                                        |                        | ~~~~                                   |                             | araraaa.    | maaaaa maaam             |  |  |
|                                        | 4131                                                                         | GGGAACAAAA                                        | GCTGGGTACC                                   | GGGCCCCCC              | TCGAGGTCAT                             | TCATATGCTT                  | GAGAAGAGAG  | TCGGGATAGT               |  |  |
|                                        | 4201                                                                         | CCAAAATAAA                                        | ACAAAGGTAA                                   | GATTACCTGG             | TCAAAAGTGA                             | AAACATCAGT                  | TAAAAGGTGG  | TATAAGTAAA               |  |  |
| la.da                                  | 4271                                                                         | ATATCGGTAA                                        | TAAAAGGTGG                                   | CCCAAAGTGA             | AATTTACTCT                             | TTTCTACTAT                  |             | GAGGATGTTT               |  |  |
| M                                      | 4341                                                                         | TGTCGGTACT                                        | TTGATACGTC                                   | ATTTTTGTAT             | GAATTGGTTT                             | TTAAGTTAL                   | TCGCGATIIO  | GAAATGCATA               |  |  |
|                                        | 4411                                                                         | TCTGTATTTG                                        | AGTCGGTTTI                                   | TAAGTTCGTT             | GCTTTTGTAA                             | ATACAGAGGG                  | ECORI       | GAAATATCTT               |  |  |
| l.i.                                   |                                                                              |                                                   |                                              |                        |                                        |                             | ECOR1       |                          |  |  |
|                                        |                                                                              |                                                   |                                              |                        |                                        | ייית איים איים איים.        |             |                          |  |  |
|                                        | 4481                                                                         | TAAAAAACCC                                        | ATATGCTAAT                                   | TTGACATAAT             | T TITICACAAA                           | · CCCupututu<br>· varvivivi | TCTAGTAAA   | CCACAATGAA<br>TAAAAGATAA |  |  |
|                                        | 4551                                                                         | CAATAATAAG                                        | ATTAAAATAG                                   | A CIIGGGG              | TIGCAGCGA                              | CTABACCCCA                  | AAGTGCTATO  | CACGATCCAT               |  |  |
|                                        | 4621                                                                         | ACTTAGACTC                                        | : AAAACATTTF                                 | A GGGA A GGG           | A CCCIAAAGIC                           | CTAAAGCCG                   | CTGGCAAATA  | A GTCTCCACCC             |  |  |
|                                        | 4691                                                                         | AGCAAGCCCA                                        | GCCCAACCCA                                   | ACCCAACCCA             | ACCCACCCCA                             | TCCCACCCA                   | AAAAAAAAA   | AGAAAGAAAA               |  |  |
|                                        | 4761                                                                         | CCGGCACTAT                                        | CACCGIGAGI                                   | TGICCGCACC             | CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC | GGCCGGAAA                   | GCGAGGAGG   | A TCGCGAGCAG             |  |  |
|                                        | 4831                                                                         | AAAAGAAAAA                                        | GAAAAACAGC                                   | , MGGIGGGIC            | A AACAAACCCC                           | CCCCATCGC                   | ACTATATACA  | A TACCCCCCC              |  |  |
|                                        | 4901                                                                         | CGACGAGGCC                                        | TOGGCCCTCCC                                  | COTACCACO              | A CCACCACCA                            | CACCTCCTC                   | CCCCTCGCTC  | G CCGGACGACG             |  |  |
|                                        | 4971                                                                         | TCTCCTCCCA                                        | A COCCCCAAC                                  | CCIACCACC              | CCACCACCAC                             | CCCGCCCCTC                  | TCCTCTTTC   | TTCTCCGTTT               |  |  |
|                                        | 5041                                                                         | AGCTCCTCCC                                        |                                              |                        | TTGGTAGTT                              | r GGGTGGGCGA                | A GAGCGGCTT | C GTCGCCCAGA             |  |  |
|                                        | 5111                                                                         | TTTTTTTCG1                                        | r Cicedicice                                 | AICITIGGC              | 0 1100171011                           | . 000100000                 | Bat         | mHI                      |  |  |
|                                        | 5181 TCGGTGCGCG GGAGGGGCGG GATCTCGCGG CTGGCGTCTC CGGGCGTGAG TCGGCCCGGA TCCTC |                                                   |                                              |                        |                                        |                             |             |                          |  |  |
|                                        | 5181                                                                         | TCGGTGCGC                                         | GGAGGGGCG                                    | GATCTCGCG              | G CTGGCGTCT                            | C CGGGCGTGA                 | F TCGGCCCGG | A TCCTCGCGGG             |  |  |
|                                        |                                                                              |                                                   | I                                            | BglII                  |                                        |                             |             |                          |  |  |
|                                        |                                                                              | G. 3.E.G.G.G.G.G.G.                               |                                              | ~~~~~<br>\             | ար Հուրարարժարագրություն               | r ጥጥጥረጥ <b>ረ</b> ርጥΔ(       | AATTTGAAT   | C CCTCAGCATT             |  |  |
|                                        | 5251                                                                         | GAATGGGGC                                         | L CICGGATGTA                                 | L THILLY THE A         | T GTGACAAAT                            | G CAGCCTCGT                 | G CGGAGCTTT | T TTGTAGC                |  |  |
|                                        | 5321                                                                         | GTTCATCGG                                         | I AGIIIICI                                   | LICAIGAII              | I CICHOHUMI                            | _ 0110001001                |             |                          |  |  |
|                                        |                                                                              |                                                   |                                              |                        |                                        |                             |             |                          |  |  |

### Figure 50 A

### Actin promoter -FAEs

Bam HI (1095) BglII(1127)pCOR deletion Xh o 1 (17) Hin d III (1248) Eco R1 (393) FULL Kpnl-EcoRI deletion Ncol(1255) Kpn I (6) ACTIN-PROMOTER-FAEs 1259 bo XhoI KpnI 1 GGTACCGGC CCCCCTCGA GGTCATTCAT ATGCTTGAGA AGAGAGTCGG GATAGTCCAA AATAAAACAA CCATGGCCCG GGGGGGAGCT CCAGTAAGTA TACGAACTCT TCTCTCAGCC CTATCAGGTT TTATTTTGTT 71 AGGTAAGATT ACCTGGTCAA AAGTGAAAAC ATCAGTTAAA AGGTGGTATA AGTAAAATAT CGGTAATAAA TCCATTCTAA TGGACCAGTT TTCACTTTTG TAGTCAATTT TCCACCATAT TCATTTTATA GCCATTATTT 141 AGGTGGCCCA AAGTGAAATT TACTCTTTC TACTATTATA AAAATTGAGG ATGTTTTGTC GGTACTTTGA TCCACCGGGT TTCACTTTAA ATGAGAAAAG ATGATAATAT TTTTAACTCC TACAAAACAG CCATGAAACT 211 TACGTCATTT TTGTATGAAT TGGTTTTTAA GTTTATCGC GATTTGGAAA TGCATATCTG TATTTGAGTC ATGCAGTAAA AACATACTTA ACCAAAAATT CAAATAAGCG CTAAACCTTT ACGTATAGAC ATAAACTCAG 281 GGTTTTTAAG TTCGTTGCTT TTGTAAATAC AGAGGGATTT GTATAAGAAA TATCTTTAAA AAACCCATAT CCAAAAATTC AAGCAACGAA AACATTTATG TCTCCCTAAA CATATTCTTT ATAGAAATTT TTTGGGTATA EcoRI ~~~~~ 351 GCTAATTTGA CATAATTTTT GAGAAAAATA TATATTCAGG CGAATTCCAC AATGAACAAT AATAAGATTA CGATTAAACT GTATTAAAAA CTCTTTTTAT ATATAAGTCC GCTTAAGGTG TTACTTGTTA TTATTCTAAT 421 AAATAGCTTG CCCCCGTTGC AGCGATGGGT ATTTTTTCTA GTAAAATAAA AGATAAACTT AGACTCAAAA TTTATCGAAC GGGGGCAACG TCGCTACCCA TAAAAAAGAT CATTTTATTT TCTATTTGAA TCTGAGTTTT 561 AACCCAACCC AACCCAACCC ACCCCAGTGC AGCCAACTGG CAAATAGTCT CCACCCCCGG CACTATCACC TTGGGTTGGG TTGGGTTCACG TCGGTTGACC GTTTATCAGA GGTGGGGGCC GTGATAGTGG CACTCAACAG GCGTGGTGGC GTGCAGAGCG TCGGTTTTTT TTTTTTTCTT TCTTTTTTTT CTTTTTCTTT 701 AACAGCAGGT GGGTCCGGGT CGTGGGGGCC GGAAAAGCGA GGAGGATCGC GAGCAGCGAC GAGCCCCGGC

TTGTCGTCCA CCCAGGCCCA GCACCCCCGG CCTTTTCGCT CCTCCTAGCG CTCGTCGCTG CTCCGGGCCG

### Figure 50 B

771 CCTCCCTCCG CTTCCAAAGA AACGCCCCCC ATCGCCACTA TATACATACC CCCCCTCTC CTCCCATCCC GGAGGGAGGC GAAGGTTTCT TTGCGGGGGG TAGCGGTGAT ATATGTATGG GGGGGAGAG GAGGGTAGGG 841 CCCAACCCTA CCACCACCAC CACCACCAC TCCTCCCCC TCGCTGCCGG ACGACGAC CCTCCCCCCT GGGTTGGGAT GGTGGTGGTG GTGGTGGTGG AGGAGGGGGG AGCGACGGCC TGCTGCTCGA GGAGGGGGGA 911 CCCCCTCCGC CGCCGCCGGT AACCACCCCG CCCCTCTCT CTTTCTTTCT CCGTTTTTT TTTCGTCTCG GGGGGAGGCG GCGGCGCCA TTGGTGGGGC GGGGAGAGGA GAAAGAAAGA GGCAAAAAAA AAAGCAGAGC 981 GTCTCGATCT TTGGCCTTGG TAGTTTGGGT GGGCGAGAGC GGCTTCGTCG CCCAGATCGC TGCGCGGGAG CAGAGCTAGA AACCGGAACC ATCAAACCCA CCCGCTCTCG CCGAAGCAGC GGGTCTAGCC ACGCGCCCTC BamHI 1051 GGGCGGGATC TCGCGGCTGG CGTCTCCGGG CGTGAGTCGG CCCGGATCCT CGCGGGGAAT GGGGCTCTCG CCCGCCCTAG AGCGCCGACC GCAGAGGCCC GCACTCAGCC GGGCCTAGGA GCGCCCCTTA CCCCGAGAGC BglII ~~~~~ 1121 GATGTAGATC TTCTTTCTTT CTTCTTTTTG TGGTAGAATT TGAATCCCTC AGCATTGTTC ATCGGTAGTT CTACATCTAG AAGAAAGAAA GAAGAAAAAC ACCATCTTAA ACTTAGGGAG TCGTAACAAG TAGCCATCAA HindIII NcoI ~~~~~~ ~~~~ 1191 TTTCTTTCA TGATTTGTGA CAAATGCAGC CTCGTGCGGA GCTTTTTTGT AG**GTAG**AAGC TTACCATGG AAAGAAAAGT ACTAAACACT GTTTACGTCG GAGCACGCCT CGAAAAAACA TCCATCTTCG AATGGTACC

Kpn1-EcoR1 - deletion underlined and restored NCO site in bold in vectors pJQ4.9, pJQ3.2 and pJO6.3.

### Figure 51

### ALEURAIN\_deleted NPIR (Apoplast) structure and sequence

Ncol (9)

Hind III (2)

ALE-CUT

Notl (87)

ALEURAIN-NPIR-DEL

93 bp

+1 M A H A R V L L L A L A V L A T A A V A HindIII Ncol

1 AAGCTTACCA TGGCCCACGC CCGCGTCCTC CTCCTGGCGC TCGCCGTGCT GGCCACGGCC GCCGTCGCCG
TTCGAATGGT ACCGGGTGCG GGCGCAGGAG GAGGACCGCG AGCGGCACGA CCGGTGCCGG CGGCAGCGGC

+1 V A S S R A A NotI

71 TCGCCTCCTC CCGCGCGGCC GCC AGCGGAGGAG GGCGCGCCGG CGG

## Figure 52

### SEE1 (Senescence enhanced) PROMOTER sequence

| PStI XbaI XbaI  71 AGCTCCGAGT TCTGACTGCA GTCTGGATGA CGCGTGTTGT ATCTAGAACT CTAGATAGCA CAGCCACAGC 141 ACCTACAGGA GTGCGACACT TGTGGACTGT AGTAGTTG GAGACGGAGC TCTTTCCTAC CTCCTGACGT 211 TGCCGCCGTT GTCCATTCCA ACGGCATCAC TCTCAACCAA TCACGCGCTC CCAACAAAAT ATCGTCCCCC 281 ATGTCTTGGC GGAGAGAGG TACATACATG CTGTCGCGC GTTTTTGTCT GAATCTCGCT TCCACTGGCC  SmaI  351 AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA 421 TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT  SphI  491 TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG 561 TTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG 631 CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT  PStI | 1    | CATGGGCCAG | GTATAATTAT | GGGATATCTC | AAGCAAATAA | TCGAAATATC            | ACCATTGGCT | ACAATATCTG |  |  |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|------------|------------|------------|------------|-----------------------|------------|------------|--|--|
| AGCTCCGAGT TCTGACTGCA GTCTGGATGA CGCGTGTTGT ATCTAGAACT CTAGATAGCA CAGCCACAGC 141 ACCTACAGGA GTGCGACACT TGTGGACTGT AGTAGTGTTG GAGACGGAGC TCTTTCCTAC CTCCTGACGT 211 TGCCGCCGTT GTCCATTCCA ACGGCATCAC TCTCAACCAA TCACGCGCTC CCAACAAAAT ATCGTCCCCC 281 ATGTCTTGGC GGAGAGAGA TACATACATG CTGTCGCGCC GTTTTTGTCT GAATCTCGCT TCCACTGGCC  Smal  351 AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA 421 TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT  Sphl  491 TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG 561 TTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG 631 CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                       |      |            | PstI       |            |            | XbaI X                | KbaI       |            |  |  |
| ACCTACAGGA GTGCGACACT TGTGGACTGT AGTAGTGTTG GAGACGGAGC TCTTTCCTAC CTCCTGACGT TGCCGCCGTT GTCCATTCCA ACGGCATCAC TCTCAACCAA TCACGCGCTC CCAACAAAAT ATCGTCCCCC ATGTCTTGGC GGAGAGAGA TACATACATG CTGTCGCGCC GTTTTTGTCT GAATCTCGCT TCCACTGGCC Smal  AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT Sphl TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG TTTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                      |      |            | ~~~~       | ~~         |            | ~~~~~~                | ~~~~       |            |  |  |
| TGCCGCCGTT GTCCATTCCA ACGGCATCAC TCTCAACCAA TCACGCGCTC CCAACAAAAT ATCGTCCCCC ATGTCTTGGC GGAGAGAGAG TACATACATG CTGTCGCGC GTTTTTGTCT GAATCTCGCT TCCACTGGCC Smal  AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT Sphl  TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG TTTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                  | 71   | AGCTCCGAGT | TCTGACTGCA | GTCTGGATGA | CGCGTGTTGT | ATCTAGAACT            | CTAGATAGCA | CAGCCACAGC |  |  |
| ATGTCTTGGC GGAGAGAGA TACATACATG CTGTCGCGC GTTTTTGTCT GAATCTCGCT TCCACTGGCC  Smal  351 AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA 421 TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT  Sphl  TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG 561 TTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG 631 CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                               | 141  | ACCTACAGGA | GTGCGACACT | TGTGGACTGT | AGTAGTGTTG | GAGACGGAGC            | TCTTTCCTAC | CTCCTGACGT |  |  |
| Smal  351 AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA 421 TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT  Sphl  TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG 561 TTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG 631 CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                                                                                                           | 211  | TGCCGCCGTT | GTCCATTCCA | ACGGCATCAC | TCTCAACCAA | TCACGCGCTC            | CCAACAAAAT | ATCGTCCCCC |  |  |
| AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT SphI TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG TTTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                                                                                                                                  | 281  | ATGTCTTGGC | GGAGAGAGAG | TACATACATG | CTGTCGCGCC | ${\tt GTTTTTGTCT}$    | GAATCTCGCT | TCCACTGGCC |  |  |
| AATCAGCTCA GCTCCCGGGA GCTCACTCAT TCAAGATCCC ATCGTCGTCG TCACCCCTGG CGTCATGGGA TGGAAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT SphI TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG TTTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                                                                                                                                  |      |            | SmaI       |            |            |                       |            |            |  |  |
| TGGAAAGAA CCTCCGTTGC TCGGATGAGT CAGCCATATC CCCGAACAGA GTACTGCAAG ATAACCCAAT  SphI  TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG  TTTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG  CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                            |      |            | ~~~~~      |            |            |                       |            |            |  |  |
| SphI  TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG  TTTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG  CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 351  | AATCAGCTCA | GCTCCCGGGA | GCTCACTCAT | TCAAGATCCC | ATCGTCGTCG            | TCACCCCTGG | CGTCATGGGA |  |  |
| TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG  TTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG  CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 421  | TGGAAAAGAA | CCTCCGTTGC | TCGGATGAGT | CAGCCATATC | CCCGAACAGA            | GTACTGCAAG | ATAACCCAAT |  |  |
| TCAGATTCCC CCAATAGAGA AAGTATAGCA TGCTTTCGGG TTTTGTTTGG CTTAATTGAC TTTATTTTTG  TTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG  CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |      |            |            | Spl        | ηΙ         |                       |            |            |  |  |
| TTGGAGTTGA ATGCTGATTT GTTGTGTAAA ATGCCCAACC ATCTGAATAT CGAGACGGAT AATAGGCTGG CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |      |            |            | ~~~        | ~~~        |                       |            |            |  |  |
| 631 CTAATTAATT TATAGCAAGA TTCTGTAGTG CACATCGCAA ATATCTTTCT GGGCATTACA GCTGGAGGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 491  | TCAGATTCCC | CCAATAGAGA | AAGTATAGCA | TGCTTTCGGG | $\mathtt{TTTTGTTTGG}$ | CTTAATTGAC | TTTATTTTTG |  |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 561  | TTGGAGTTGA | ATGCTGATTT | GTTGTGTAAA | ATGCCCAACC | ATCTGAATAT            | CGAGACGGAT | AATAGGCTGG |  |  |
| PstI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 631  | CTAATTAATT | TATAGCAAGA | TTCTGTAGTG | CACATCGCAA | ATATCTTTCT            | GGGCATTACA | GCTGGAGGCT |  |  |
| ~~~~~                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | PstI |            |            |            |            |                       |            |            |  |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |      |            |            |            |            |                       |            |            |  |  |
| 701 TCATCAGCCT GAAACACTCT GCAGAGCCTG AAGCAAGTGG TGAAGCGTGG CGATGAGATG GGTATAAAAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 701  | TCATCAGCCT | GAAACACTCT | GCAGAGCCTG | AAGCAAGTGG | TGAAGCGTGG            | CGATGAGATG | GGTATAAAAC |  |  |
| 771 CCCCGGCACC GGGACGCGAG CTCCCGCCTA CCAGTACCAT CTCGCCTCGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 771  | CCCCGGCACC | GGGACGCGAG | CTCCCGCCTA | CCAGTACCAT | CTCGCCTCGC            | TCCCCCTGCC | GGACGACCCA |  |  |
| 841 GTAAAATACT GTTGCCCACT CGCCGGCGAG ATG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 841  | GTAAAATACT | GTTGCCCACT | CGCCGGCGAG | ATG        |                       |            |            |  |  |

### Figure <u>53</u>

### SEE1 (Senescence enhanced) PROMOTER plus vacuolar aleurain SIGNAL/NPIR sequence

| 1   | CATGGGCCAG | ${\tt GTATAATTAT}$ | GGGATATCTC | AAGCAAATAA         | TCGAAATATC | ACCATTGGCT | ACAATATCTG |
|-----|------------|--------------------|------------|--------------------|------------|------------|------------|
|     |            | PstI               |            |                    | XbaI I     | KbaI       |            |
|     |            | ~~~~               | ~~         |                    | ~~~~~~ ~   | ~~~~       |            |
| 71  | AGCTCCGAGT | TCTGACTGCA         | GTCTGGATGA | CGCGTGTTGT         | ATCTAGAACT | CTAGATAGCA | CAGCCACAGC |
| 141 | ACCTACAGGA | GTGCGACACT         | TGTGGACTGT | AGTAGTGTTG         | GAGACGGAGC | TCTTTCCTAC | CTCCTGACGT |
| 211 | TGCCGCCGTT | GTCCATTCCA         | ACGGCATCAC | TCTCAACCAA         | TCACGCGCTC | CCAACAAAAT | ATCGTCCCCC |
| 281 | ATGTCTTGGC | GGAGAGAGAG         | TACATACATG | CTGTCGCGCC         | GTTTTTGTCT | GAATCTCGCT | TCCACTGGCC |
|     |            | SmaI               |            |                    |            |            |            |
|     |            | ~~~~~~             |            |                    |            |            |            |
| 351 | AATCAGCTCA | GCTCCCGGGA         | GCTCACTCAT | TCAAGATCCC         | ATCGTCGTCG | TCACCCCTGG | CGTCATGGGA |
| 421 | TGGAAAAGAA | CCTCCGTTGC         | TCGGATGAGT | CAGCCATATC         | CCCGAACAGA | GTACTGCAAG | ATAACCCAAT |
|     |            |                    | Spl        | nI                 |            |            |            |
|     |            |                    | ~~~        | ~~~                |            |            |            |
| 491 | TCAGATTCCC | CCAATAGAGA         | AAGTATAGCA | TGCTTTCGGG         | TTTTGTTTGG | CTTAATTGAC | TTTATTTTTG |
| 561 | TTGGAGTTGA | ATGCTGATTT         | GTTGTGTAAA | ATGCCCAACC         | ATCTGAATAT | CGAGACGGAT | AATAGGCTGG |
| 631 | CTAATTAATT | TATAGCAAGA         | TTCTGTAGTG | CACATCGCAA         | ATATCTTTCT | GGGCATTACA | GCTGGAGGCT |
|     |            | Ps                 | stI        |                    |            |            |            |
|     |            | ~~                 | ~~~~       |                    |            |            |            |
| 701 | TCATCAGCCT | GAAACACTCT         | GCAGAGCCTG | ${\tt AAGCAAGTGG}$ | TGAAGCGTGG | CGATGAGATG | GGTATAAAAC |
| 771 | CCCCGGCACC | GGGACGCGAG         | CTCCCGCCTA | CCAGTACCAT         | CTCGCCTCGC | TCCCCCTGCC | GGACGACCCA |
|     |            |                    |            | MAHO               | G RIL      | F L A      | L A V L    |
| 841 | GTAAAATACT | GTTGCCCACT         | CGCCGGCGAG | ATGGCCCACG         | GCCGCATCCT | CTTCTTGGCG | CTCGCCGTCT |
|     |            |                    |            |                    |            |            | BssHII     |
|     |            |                    |            |                    |            |            | NotI       |
|     | · A T A    | A V A              | A A S 1    | L A D S            | N P I      | R P V 7    | r era·     |
| 911 | TGGCCACCGC | CGCGGTGGCC         | GCCGCATCNT | TGGCGGACTC         | CAACCCGATC | CGGCCCGTCA | CCGAGCGCGC |
|     | NotI       |                    |            |                    |            |            |            |
|     | ~~~~~      |                    |            |                    |            |            |            |
|     | - A A      |                    |            |                    |            |            |            |
| 981 | GGCCGCC    |                    |            |                    |            |            |            |
|     |            |                    |            |                    |            |            |            |